

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.



- (ii) TITLE OF INVENTION: Human Telomerase Catalytic Subunit
- (iii) NUMBER OF SEQUENCES: 727
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/974,549
(B) FILING DATE: 19-NOV-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/851,843
(B) FILING DATE: 06-MAY-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/854,050
(B) FILING DATE: 09-MAY-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/911,312
(B) FILING DATE: 14-AUG-1997

- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/912,951
 (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/915,503
 (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: WO PCT/US97/17618
 (B) FILING DATE: 01-OCT-1997
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: WO PCT/US97/17885
 (B) FILING DATE: 01-OCT-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Apple, Randolph Ted
 (B) REGISTRATION NUMBER: 36,429
 (C) REFERENCE/DOCKET NUMBER: 015389-002610US
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4015 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 56..3454
 (D) OTHER INFORMATION: /product= "hTRT"
 /note= "human telomerase reverse
 transcriptase (hTRT) catalytic protein
 component"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC							106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His							
	5		10		15		
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC							154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro							
	20		25		30		

CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala 35 40 45	202
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CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val 70 75 80	298
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu 85 90 95	346
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu 100 105 110	394
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp 115 120 125	442
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
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CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
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GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
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CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874

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GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355 360 365	1162
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg 370 375 380 385	1210
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CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala 405 410 415	1306
GGG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly 420 425 430	1354
TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val 435 440 445	1402
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val 450 455 460 465	1450
CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg 470 475 480	1498
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu 485 490 495	1546
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500 505 510	1594

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CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550 555 560	1738
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AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595 600 605	1882
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AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
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ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314

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770					775					780					785	
CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	TCC	CTG	AAT	GAG	GCC	2458
Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	Ala	
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AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CGC	TTC	ATG	TGC	CAC	CAC	GCC	2506
Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	
			805					810					815			
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Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	
		820					825					830				
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Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	
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GAG	AAC	AAG	CTG	TTT	GCG	GGG	ATT	CGG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	2650
Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	
850					855					860					865	
TTG	GTG	GAT	GAT	TTC	TTG	TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	2698
Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	
				870					875					880		
ACC	TTC	CTC	AGG	ACC	CTG	GTC	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	2746
Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	
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Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	
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Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	
	915					920					925					
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Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	
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Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	Asn	
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CGC	GGC	TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA	CTC	TTT	GGG	GTC	2986
Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	
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TCCACCCCAG GGCCAGCTTT TCCTCACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
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AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAAT ACTGAATATA TGAGTTTTTC AGTTTTGAAA	4011
AAAA	4015

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
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Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
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Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
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Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
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Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
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Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
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Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
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Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
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Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
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Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
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 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
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 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
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 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
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 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
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 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
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 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2176
- (D) OTHER INFORMATION: /note= "clone 712562"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 23..802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCAAGTTC CTGCACTGGC TGATGAGTGT GTACGTCGTC GAGCTGCTCA GGTCTTTCTT	60
TTATGTCACG GAGACCACGT TTCAAAAGAA CAGGCTCTTT TTCTACCGGA AGAGTGTCTG	120
GAGCAAGTTG CAAAGCATTG GAATCAGACA GCACTTGAAG AGGGTGCAGC TGCGGGAGCT	180
GTCGGAAGCA GAGGTCAGGC AGCATCGGGA AGCCAGGCCC GCCCTGCTGA CGTCCAGACT	240
CCGCTTCATC CCCAAGCCTG ACGGGCTGCG GCCGATTGTG AACATGGACT ACGTCGTGGG	300
AGCCAGAACG TTCCGCAGAG AAAAGAGGGC CGAGCGTCTC ACCTCGAGGG TGAAGGCACT	360
GTTCAGCGTG CTCAACTACG AGCGGGCGCG GCGCCCCGGC CTCCTGGGCG CCTCTGTGCT	420
GGGCCTGGAC GATATCCACA GGGCCTGGCG CACCTTCGTG CTGCGTGTGC GGGCCAGGA	480
CCCGCCGCCT GAGCTGTACT TTGTCAAGGT GGATGTGACG GGCGCGTACG ACACCATCCC	540
CCAGGACAGG CTCACGGAGG TCATCGCCAG CATCATCAAA CCCCAGAACA CGTACTGCGT	600
GCCTCGGTAT GCCGTGGTCC AGAAGGCCGC CCATGGGCAC GTCCGCAAGG CCTTCAAGAG	660
CCACGTCCTA CGTCCAGTGC CAGGGGATCC CGCAGGGCTC CATCCTCTCC ACGCTGCTCT	720
GCAGCCTGTG CTACGGCGAC ATGGAGAACA AGCTGTTTGC GGGGATTCCG CGGGACGGGC	780
TGCTCTGCG TTTGGTGGAT GATTTCTTGT TGGTGACACC TCACCTCACC CACGCGAAAA	840
CCTTCCTCAG GACCCTGGTC CGAGGTGTCC CTGAGTATGG CTGCGTGGTG AACTTGCGGA	900
AGACAGTGGT GAACTTCCCT GTAGAAGACG AGGCCCTGGG TGGCACGGCT TTTGTTCAGA	960
TGCGGGCCCA CGGCCTATTC CCCTGGTGCG GCCTGCTGCT GGATACCCGG ACCCTGGAGG	1020
TGCAGAGCGA CTA CTCCAGC TATGCCCGGA CCTCCATCAG AGCCAGTCTC ACCTTCAACC	1080
GCGGCTTCAA GGCTGGGAGG AACATGCGTC GCAAACCTTT TGGGGTCTTG CGGCTGAAGT	1140
GTCACAGCCT GTTTCTGGAT TTGCAGGTGA ACAGCCTCCA GACGGTGTGC ACCAACATCT	1200
ACAAGATCCT CCTGCTGCAG GCGTACAGGT TTCACGCATG TGTGCTGCAG CTCCCATTTC	1260
ATCAGCAAGT TTGGAAGAAC CCCACATTTT TCCTGCGCGT CATCTCTGAC ACGGCCTCCC	1320
TCTGCTACTC CATCCTGAAA GCCAAGAACG CAGGGATGTC GCTGGGGGCC AAGGGCGCCG	1380
CCGGCCNTCT GCCCTCCGAG GCCGTGCAGT GGCTGTGCCA CCAAGCATTG CTGCTCAAGC	1440
TGACTCGACA CCGTGTCAAC TACGTGCCAC TCCTGGGGTC ACTCAGGACA GCCCAGACGC	1500
AGCTGAGTCG GAAGCTCCCG GGGACGACGC TGA CTGCCCT GGAGCCGCA GCCAACCCGG	1560
CACTGCCCTC AGACTTCAAG ACCATCCTGG ACTGATGGCC ACCCGCCCAC AGCCAGGCCG	1620

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AGAGCAGACA CCAGCAGCCC TGTCACGCCG GGCTCTACGT CCCAGGGAGG GAGGGGCGGC      1680
CCACACCCAG GCCTGCACCG CTGGGAGTCT GAGGCCTGAG TGAGTGTTTG GCCGAGGCCT      1740
GCATGTCCGG CTGAAGGCTG AGTGTCCGGC TGAGGCCTGA GCGAGTGTCC AGCCAAGGGC      1800
TGAGTGTCCA GCACACCTGC CGTCTTCACT TCCCCACAGG CTGGCGCTCG GCTCCACCCC      1860
AGGGCCAGCT TTCCTCACC AGGAGCCCGG CTTCCACTCC CCACATAGGA ATAGTCCATC      1920
CCCAGATTCG CCATTGTTCA CCCCTCGCCC TGCCCTCCTT TGCCTTCCAC CCCCACCATC      1980
CAGGTGGAGA CCCTGAGAAG GACCCTGGGA GCTCTGGGAA TTTGGAGTGA CCAAAGGTGT      2040
GCCCTGTACA CAGGCGAGGA CCCTGCACCT GGATGGGGGT CCCTGTGGGT CAAATTGGGG      2100
GGAGGTGCTG TGGGAGTAAA ATACTGAATA TATGAGTTTT TCAGTTTTGN AAAAAAAAAA      2160
AAAAAAAAAA AAAAAA                                     2176

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3855
- (D) OTHER INFORMATION: /note= "nucleic acid sequence with an open reading frame encoding a delta-182 variant polypeptide"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..2479
- (D) OTHER INFORMATION: /product= "delta-182 variant polypeptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG      58
                                     Met
                                     1
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC      106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
      5                      10                      15
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC      154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
      20                      25                      30

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CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala 35 40 45	202
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro 50 55 60 65	250
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val 70 75 80	298
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu 85 90 95	346
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu 100 105 110	394
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp 115 120 125	442
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu 150 155 160	538
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln 165 170 175	586
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874

TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC	922
Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu	
275 280 285	
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG	970
Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala	
290 295 300 305	
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT	1018
Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys	
310 315 320	
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC	1066
Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp	
325 330 335	
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC	1114
Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser	
340 345 350	
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG	1162
Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg	
355 360 365	
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC	1210
Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg	
370 375 380 385	
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG	1258
Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala	
390 395 400	
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT	1306
Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala	
405 410 415	
GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC	1354
Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly	
420 425 430	
TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG	1402
Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val	
435 440 445	
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG	1450
Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val	
450 455 460 465	
CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG	1498
Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg	
470 475 480	
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG	1546
His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu	
485 490 495	
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC	1594
Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser	
500 505 510	

GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515 520 525	1642
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu 530 535 540 545	1690
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550 555 560	1738
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg 565 570 575	1786
AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu 580 585 590	1834
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595 600 605	1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610 615 620 625	1930
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314

CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA GTG CCA GGG His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly 755 760 765	2362
GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG CAG CCT GTG CTA Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu 770 775 780 785	2410
CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT TCG GCG GGA CGG GCT Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala 790 795 800	2458
GCT CCT GCG TTT GGT GGA TGATTCTTG TTGGTGACAC CTCACCTCAC Ala Pro Ala Phe Gly Gly 805	2506
CCACGCGAAA ACCTTCCTCA GGACCCTGGT CCGAGGTGTC CCTGAGTATG GCTGCGTGGT	2566
GAACCTTGCGG AAGACAGTGG TGAACCTCCC TGTAAGAAGAC GAGGCCCTGG GTGGCACGGC	2626
TTTTGTTTCTAG ATGCCGGGCC ACGGCCTATT CCCCTGGTGC GGCCTGCTGC TGGATACCCG	2686
GACCCTGGAG GTGCAGAGCG ACTACTCCAG CTATGCCCGG ACCTCCATCA GAGCCAGTCT	2746
CACCTTCAAC CGCGGCTTCA AGGCTGGGAG GAACATGCGT CGCAAACCTCT TTGGGGTCTT	2806
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CACGGCCTCC CTCTGCTACT CCATCCTGAA AGCCAAGAAC GCAGGGATGT CGCTGGGGGC	3046
CAAGGGCGCC GCGGGCCCTC TGCCCTCCGA GGCCGTGCAG TGGCTGTGCC ACCAAGCATT	3106
CCTGCTCAAG CTGACTCGAC ACCGTGTCAC CTACGTGCCA CTCCTGGGGT CACTCAGGAC	3166
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CAGCCAGGCC GAGAGCAGAC ACCAGCAGCC CTGTCACGCC GGGCTCTACG TCCCAGGGAG	3346
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AATAGTCCAT CCCCAGATTC GCCATTGTTC ACCCCTCGCC CTGCCCTCCT TTGCCTTCCA	3646
CCCCCACCAT CCAGGTGGAG ACCCTGAGAA GGACCCTGGG AGCTCTGGGA ATTTGGAGTG	3706
ACCAAAGGTG TGCCCTGTAC ACAGGCGAGG ACCCTGCACC TGGATGGGGG TCCCTGTGGG	3766
TCAAATTGGG GGGAGGTGCT GTGGGAGTAA AATACTGAAT ATATGAGTTT TTCAGTTTGG	3826
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3855

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1           5           10           15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20           25           30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35           40           45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50           55           60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65           70           75           80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85           90           95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100           105           110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115           120           125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130           135           140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145           150           155           160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165           170           175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180           185           190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195           200           205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210           215           220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225           230           235           240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245           250           255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260           265           270

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Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro
 755 760 765
 Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val
 770 775 780
 Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg
 785 790 795 800
 Ala Ala Pro Ala Phe Gly Gly
 805

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..4335
- (D) OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 2715..2818
- (D) OTHER INFORMATION: /note= "intron 1"

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 4173..4326
- (D) OTHER INFORMATION: /note= "intron 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCATGGGACC CACTGCAGGG GCAGCTGGGA GGCTGCAGGC TTCAGGTCCC AGTGGGGTTG	60
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CTCAATGTCT CAGTGTGTGC TGAAACATGT AGAAATTAAA GTCCATCCCT CCTACTCTAC	180
TGGGATTGAG CCCCTTCCCT ATCCCCCCCC AGGGGCAGAG GAGTTCCTCT CACTCCTGTG	240
GAGGAAGGAA TGATACTTTG TTATTTTTCA CTGCTGGTAC TGAATCCACT GTTTCATTTG	300
TTGGTTTGTT TGTTTTGTTT TGAGAGGCGG TTCACTCTT GTTGCTCAGG CTGGAGGGAG	360
TGCAATGGCG CGATCTTGGC TTA CTGCTGCCCT CAGGTTCAAG TGATTCTCCT	420
GCTTCCGCCT CCCATTTGGC TGGGATTACA GGCACCCGCC ACCATGCCCA GCTAATTTTT	480
TGTATTTTTA GTAGAGACGG GGGTGGGGT GGGGTTCAAC ATGTTGGCCA GGCTGGTCTC	540
GAAGTTCTGA CCTCAGATGA TCCACCTGCC TCTGCCTCCT AAAGTGCTGG GATTACAGGT	600
GTGAGCCACC ATGCCCAGCT CAGAATTTAC TCTGTTTAGA AACATCTGGG TCTGAGGTAG	660
GAAGCTCACC CCACTCAAGT GTTGTGGTGT TTTAAGCCAA TGATAGAATT TTTTATTGT	720
TGTTAGAACA CTCTTGATGT TTTACTGT GATGACTAAG ACATCATCAG CTTTTCAAAG	780
ACACACTAAC TGCACCCATA AACTGGGGT GTCTTCTGGG TATCAGCGAT CTTCAATTGAA	840
TGCGGGGAGG CGTTTCTCG CCATGCACAT GGTGTTAATT ACTCCAGCAT AATCTTCTGC	900
TTCCATTTCT TCTCTCCCT CTTTTAAAT TGTGTTTTCT ATGTTGGCTT CTCTGCAGAG	960
AACCAGTGTA AGCTACAAC TAACTTTTGT TGGAACAAAT TTTCCAAACC GCCCCTTTGC	1020
CCTAGTGGCA GAGACAATTC ACAAACACAG CCCTTTAAAA AGGCTTAGGG ATCACTAAGG	1080
GGATTTCTAG AAGAGCGACC CGTAATCCTT AAGTATTTAC AAGACGAGGC TAACCTCCAG	1140
CGAGCGTGAC AGCCCAGGGA GGGTGCGAGG CCTGTTCAAA TGCTAAGCTT CCATAAATAA	1200
AGCAAATTTT CTCCGGCAGT TTCTGGAAAG TAGGAAAGGT TAACATTTAA GGTGCGTTT	1260
GTTAGCATTT CAGTGTTTGC CGACCTCAGC TAACAGCATC CCTGCAAGGC CTCGGGAGAC	1320
CCAGAAGTTT CTCGCCCCTT AGATCCAAAC TTGAGCAACC CGGAGTCTGG ATTCCTGGGA	1380
AGTCCTCAGC TGTCTGCGG TTGTGCCGGG GCCCCAGGTC TGGAGGGGAC CAGTGGCCGT	1440

GTGGCTTCTA CTGCTGGGCT GGAAGTCGGG CCTCCTAGCT CTGCAGTCCG AGGCTTGGAG	1500
CCAGGTGCCT GGACCCCGAG GCTGCCCTCC ACCCTGTGCG GGCGGGATGT GACCAGATGT	1560
TGGCCTCATC TGCCAGACAG AGTGCCGGGG CCCAGGGTCA AGGCCGTTGT GGCTGGTGTG	1620
AGGCGCCCGG TGC CGGCCA GCAGGAGCGC CTGGCTCCAT TTCCCACCCT TTCTCGACGG	1680
GACCGCCCCG GTGGGTGATT AACAGATATT GGGGTGGTTT GTCATGGTG GGGACCCCTT	1740
CGCCGCCTGA GAACCTGCAA AGAGAAATGA CGGGCCTGTG TCAAGGAGCC CAAGTCGCGG	1800
GGAAGTGTTG CAGGGAGGCA CTCCGGGAGG TCCCGCGTGC CCGTCCAGGG AGCAATGCGT	1860
CCTCGGGTTC GTCCCCAGCC GCGTCTACGC GCCTCCGTCC TCCCCTTCAC GTCCGGCATT	1920
CGTGGTGCCC GGAGCCCGAC GCCCCGCGTC CGGACCTGGA GGCAGCCCTG GGTCTCEGGA	1980
TCAGGCCAGC GGCCAAAGGG TCGCCGCACG CACCTGTTCC CAGGGCCTCC ACATCATGGC	2040
CCCTCCCTCG GGTTACCCCA CAGCCTAGGC CGATTGACG TCTCTCCGCT GGGGCCCTCG	2100
CTGGCGTCCC TGCACCCTGG GAGCGCGAGC GGCGCGCGGG CGGGGAAGCG CGGCCAGAC	2160
CCCCGGGTCC GCCCGGAGCA GCTGCGCTGT CGGGGCCAGG CCGGGCTCCC AGTGGATTCC	2220
CGGGCAACAG ACGCCAGGA CCGCGCTTCC CACGTGGCGG AGGGACTGGG GACCCGGGCA	2280
CCGGTCCTGC CCCTTCACCT TCCAGCTCCG CCTCGTCCGC GCGGAACCCC GCCCCGTCCC	2340
GAACCCTTCC CGGGTCCCCG GCCCAGCCCC TTCCGGGCCA TCCCAGCCCG TCCCGTTCTT	2400
TTTCCGCGGC CCGGCCCTCT CCTCGCGGCG CGAGTTTCAG GCAGCGCTGC GTCTGTCTGC	2460
GCAGGTGGGA AGCCCTGGCC CCGGCCACCC CCGCGATGCC GCGCGCTCCC CGGTGCCGAG	2520
CCGTGCGCTC CCTGTGCGC AGCCACTACC GCGAGGTGCT GCGCTGGCC ACGTTCGTGC	2580
GGCGCCTGGG GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG	2640
CCCTGCTGGC CCAGTGCCTG GTGTGCGTGC CCTGGGACGC ACGGCCGCCC CCCGCGCCC	2700
CCTCCTTCCG CCAGGTGGGC CTCCCCGGGG TCGCGTCCG GCTGGGGTTG AGGGCGGGCG	2760
GGGGGAACCA GCGACATGCG GAGAGCAGCG CAGGCGACTC AGGGCGCTTC CCCCAGAGT	2820
GTCTGCCTG AAGGAGCTGG TGGCCCGAGT GCTGCAGAGG CTGTGCGAGC GCGGCGCGAA	2880
GAACGTGCTG GCCTTCGGCT TCGCGCTGCT GGACGGGGCC CGCGGGGGCC CCCCCAGGC	2940
CTTACACCACC AGCGTGCGCA GCTACCTGCC CAACACGGTG ACCGACGCAC TGCGGGGGAG	3000
CGGGGCGTGG GGGCTGCTGC TGC GCCGT GGGCGACGAC GTGCTGGTTC ACCTGCTGGC	3060
ACGCTGCGCG CTCTTTGTGC TGGTGGCTCC CAGCTGCGCC TACCAGGTGT GCGGGCCGCC	3120
GCTGTACCAG CTCGGCGCTG CCACTCAGGC CCGGCCCCCG CCACACGCTA GTGGACCCCG	3180
AAGGCGTCTG GGATGCGAAC GGGCCTGGAA CCATAGCGTC AGGGAGGCCG GGGTCCCCCT	3240
GGGCCTGCCA GCCCCGGGTG CGAGGAGGCG CGGGGGCAGT GCCAGCCGAA GTCTGCCGTT	3300

GCCCAAGAGG CCCAGGCGTG GCGCTGCCCC TGAGCCGGAG CGGACGCCCG TTGGGCAGGG	3360
GTCCTGGGCC CACCCGGGCA GGACGCGTGG ACCGAGTGAC CGTGGTTTCT GTGTGGTGTC	3420
ACCTGCCAGA CCCGCCGAAG AAGCCACCTC TTTGGAGGGT GCGCTCTCTG GCACGCGCCA	3480
CTCCACCCA TCCGTGGGCC GCCAGCACCA CGCGGGCCCC CCATCCACAT CGCGGCCACC	3540
ACGTCCCTGG GACACGCCTT GTCCCCCGGT GTACGCCGAG ACCAAGCACT TCCTCTACTC	3600
CTCAGGCGAC AAGGAGCAGC TGCGGCCCTC CTTCTACTC AGCTCTCTGA GGCCCAGCCT	3660
GACTGGCGCT CGGAGGCTCG TGGAGACCAT CTTTCTGGGT TCCAGGCCCT GGATGCCAGG	3720
GACTCCCCGC AGGTTGCCCC GCCTGCCCCA GCGCTACTGG CAAATGCGGC CCCTGTTTCT	3780
GGAGCTGCTT GGGAAACCACG CGCAGTGCCC CTACGGGGTG CTCCTCAAGA CGCACTGCCC	3840
GCTGCGAGCT GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC	3900
TGTGGCGGCC CCCGAGGAGG AGGACACAGA CCCCCGTCGC CTGGTGCAGC TGCTCCGCCA	3960
GCACAGCAGC CCCTGGCAGG TGTACGGCTT CGTGCGGGCC TGCTGCGCC GGCTGGTGCC	4020
CCCAGGCCCTC TGGGGCTCCA GGCACAACGA ACGCCGCTTC CTCAGGAACA CCAAGAAGTT	4080
CATCTCCCTG GGGAAGCATG CCAAGCTCTC GCTGCAGGAG CTGACGTGGA AGATGAGCGT	4140
GCGGGACTGC GCTTGGCTGC GCAGGAGCCC AGGTGAGGAG GTGGTGGCCG TCGAGGGCCC	4200
AGGCCCCAGA GCTGAATGCA GTAGGGGCTC AGAAAAGGGG GCAGGCAGAG CCCTGGTCCT	4260
CCTGTCTCCA TCGTCACGTG GGCACACGTG GCTTTTCGCT CAGGACGTCG AGTGGACACG	4320
GTGATCGAGG TCGAC	4335

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 95..198
- (D) OTHER INFORMATION: /note= "intron 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGACCCGGCG GCTTTCCGCG CGCTGGTGGC CCAGTGCCCTG GTGTGCGTGC CCTGGGACGC	60
ACGGCCGCCC CCCGCCGCC CCTCCTTCCG CCAGGTGGGC CTCCCCGGGG TCGGCGTCCG	120
GCTGGGGTTG AGGGCGGCCG GGGGAACCA GCGACATGCG GAGAGCAGCG CAGGCGACTC	180

AGGGCGCTTC CCCCGCAGGT GTCCTGCCTG AAGGAGCTGG TGGCCCGAGT GCTGCAGAGG 240

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: /note= "expressed sequence tag (EST)
AA281296"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCAAGTTCC TGCCTGGCT GATGAGTGTG TACGTCGTCG AGCTGCTCAG GTCTTTCTTT	60
TATGTACAGG AGACCACGTT TCAAAAGAAC AGGCTCTTTT TCTACCGGAA GAGTGTCTGG	120
AGCAAGTTGC AAAGCATTGG AATCAGACAG CACTTGAAGA GGGTGCAGCT GCGGGACGTG	180
TCGGAAGCAG AGGTCAGGCA GCATCGGGAA GCCAGGCCCG CCCTGCTGAC GTCCAGACTC	240
CGCTTCATCC CCAAGCCTGA CGGGCTGCGG CCGATTGTGA ACATGGACTA CGTCGTGGGA	300
GCCAGAACGT TCCGCAGAGA AAAGAGGGCC GAGCGTCTCA CCTCGAGGGT GAAGGCACTG	360
TTGAGCGTGC TCAACTACGA GCGGGCGCG	389

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: /note= "182 basepair sequence deleted in
clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCTACCTTGA CAGACCTCCA GCCGTACATG CGACAGTTCG TGGCTCACCT GCAGGAGACC	60
AGCCCGCTGA GGGATGCCGT CGTCATCGAG CAGAGCTCCT CCCTGAATGA GGCCAGCAGT	120

GGCCTCTTCG ACGTCTTCCT ACGCTTCATG TGCCACCACG CCGTGCGCAT CAGGGGCAAG 180
 TC 182

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..259
- (D) OTHER INFORMATION: /note= "protein encoded by clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	Thr	1	5	10	15
Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys	Ser	Val	20	25	30	
Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	Val	35	40	45	
Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	Ala	50	55	60	
Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	65	70	75	80
Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr	85	90	95	
Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	Val	Lys	Ala	100	105	110	
Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	Leu	115	120	125	
Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	Thr	130	135	140	
Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	Leu	Tyr	Phe	145	150	155	160
Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	Gln	Asp	Arg	165	170	175	
Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	180	185	190	

Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	His	Val	Arg		
		195						200					205				
Lys	Ala	Phe	Lys	Ser	His	Val	Leu	Arg	Pro	Val	Pro	Gly	Asp	Pro	Ala		
		210					215					220					
Gly	Leu	His	Pro	Leu	His	Ala	Ala	Leu	Gln	Pro	Val	Leu	Arg	Arg	His		
		225				230				235					240		
Gly	Glu	Gln	Ala	Val	Cys	Gly	Asp	Ser	Ala	Gly	Arg	Ala	Ala	Pro	Ala		
				245						250					255		
Phe	Gly	Gly															

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Trp
1           5           10           15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
          20           25           30

Xaa Trp

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Trp
1          5          10          15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
          20          25          30

Xaa Xaa Trp
          35

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: /note= "TRT motifs from human"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1          5          10          15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
          20          25          30

Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
          35          40          45

Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
          50          55          60

Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
          65          70          75          80

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
          85          90          95

```

Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 100 105 110

Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 115 120 125

Ala

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from
 Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys
 1 5 10 15

Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe
 20 25 30

Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe
 35 40 45

Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe
 50 55 60

Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met
 65 70 75 80

Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp
 85 90 95

Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys
 100 105 110

Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile
 115 120 125

Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu
 130 135 140

Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser
 145 150 155 160

Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys
 165 170 175

Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val
 180 185 190
 Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met
 195 200 205
 Phe Arg Ile Val Lys Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg
 210 215 220
 Lys Tyr Ala Thr Ile His Ala Thr Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from *Saccharomyces cerevisiae* EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys
 1 5 10 15
 His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp
 20 25 30
 Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys
 35 40 45
 Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr
 50 55 60
 Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr
 65 70 75 80
 Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser
 85 90 95
 Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
 100 105 110
 Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu
 115 120 125
 Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln
 130 135 140

Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys
 145 150 155 160
 Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln
 165 170 175
 Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met
 180 185 190
 Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys
 195 200 205
 Met Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val
 210 215 220
 Arg Ser Gln Tyr Phe Phe Asn Thr Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Euplotes aediculatus pl23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser Ala Lys His Phe
 1 5 10 15
 Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp Lys Leu Leu Arg
 20 25 30
 Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
 35 40 45
 Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 50 55 60
 Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
 65 70 75 80
 Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu Trp Lys Lys
 85 90 95
 Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr
 100 105 110

Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp
 115 120 125
 Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His
 130 135 140
 Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly
 145 150 155 160
 Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe
 165 170 175
 Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr
 180 185 190
 Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg Glu Lys Leu Ser
 195 200 205
 Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp Phe Trp Ile Met
 210 215 220
 Thr Ala Gln Ile Leu Lys Arg Lys Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif T"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly, Ser, Thr, Tyr, Cys, Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Xaa Phe Phe Tyr
 1

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..7
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Xaa Arg Xaa Ile Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif 2"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Phe Arg Xaa Ile
1

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif A"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = charged amino acid, Asp,
Glu, His, Lys or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro Xaa Leu Tyr Phe Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..6

(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif B'"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Ile Pro Gln Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..4

(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Leu Arg Leu
1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..7

(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif C"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asp Asp Phe Leu Xaa Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "motif T peptide from
Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
1 5 10 15
Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
20 25 30
Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met
35 40 45

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr Leu Pro Pro Ala Val
 1 5 10 15
 Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu
 20 25 30
 Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn Lys Lys Met Leu Val
 35 40 45
 Ser Thr Asn Gln Thr Leu
 50

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from
 Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr
 1 5 10 15
 Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys Lys Leu
 20 25 30
 Lys Asp

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from
 Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser
 1 5 10 15
 Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu
 20 25 30
 Ser Phe Thr
 35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from
 Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 1 5 10 15
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 20 25 30
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
 Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "motif T peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr
 1 5 10 15

Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys
 20 25 30

Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
 1 5 10 15

Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 20 25 30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..34
(D) OTHER INFORMATION: /note= "motif A peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Pro  Pro  Pro  Glu  Leu  Tyr  Phe  Val  Lys  Val  Asp  Val  Thr  Gly  Ala  Tyr
1      5      10     15
Asp  Thr  Ile  Pro  Gln  Asp  Arg  Leu  Thr  Glu  Val  Ile  Ala  Ser  Ile  Ile
      20     25     30
Lys  Pro

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /note= "motif B' peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser
1 5 10 15

Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe
20 25 30

Ala Gly Ile
35

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr
1				5					10					15	
His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr
			20					25					30		
Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val					
			35				40								

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu
1				5				10		

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "motif T peptide from Euplotes aediculatus pl23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1           5           10           15

Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
          20           25           30

Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
          35           40           45

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Euplotes aediculatus pl23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
1           5           10           15

Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
          20           25           30

Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
          35           40           45

Asn Thr Lys Leu Leu Asn
          50

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 1 5 10 15

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 20 25 30

Leu Leu

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser
 1 5 10 15

Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu
 20 25 30

Gly Phe Leu
 35

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
1              5              10              15
Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn
                20              25              30
Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr
                35              40

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile
1              5              10

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: /note= "motif T peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1 5 10 15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
 20 25 30

Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /note= "motif 1 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn Phe Asn His Ser Lys
1 5 10 15

Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
 20 25

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "motif 2 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
1           5           10           15
Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro
          20           25

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1           5           10           15
Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
          20           25           30
Lys Asn

```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser
 1 5 10 15
 Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser
 20 25 30
 Glu Phe Lys
 35

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
 1 5 10 15
 Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
 20 25 30
 Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Lys Glu Leu Glu Val Trp Lys His Ser Ser Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..4
(D) OTHER INFORMATION: /note= "consensus non-telomerase RT
sequence from motif B"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Xaa Pro Gln Gly
1

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..5
(D) OTHER INFORMATION: /note= "consensus non-telomerase RT
sequence from motif C"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Asp Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Leu Ser Asn Glu Leu Gly Thr Gly Lys Phe Lys Phe Lys Pro Met Arg
1 5 10 15

Ile Val Asn Ile Pro Lys Pro Lys Gly Gly Ile Arg Pro Leu Ser Val
20 25 30

Gly Asn Pro Arg Asp Lys Ile Val Gln Glu Val Met Arg Met Ile Leu
35 40 45

Asp Thr Ile Phe Asp Lys Lys
50 55

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Phe Gly Gly Ser Asn Trp Phe Ile Glu Val Asp Leu Lys Lys Cys Phe
1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Thr Tyr His Lys Pro Met Leu Gly Leu Pro Gln Gly Ser Leu Ile Ser
1 5 10 15

Pro Ile Leu Cys Asn Ile Val Met Thr Leu Val Asp Asn Trp Leu Glu
20 25 30
Asp Tyr Ile
35

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /note= "motif C peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys
1 5 10 15
Asn

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..25
(D) OTHER INFORMATION: /note= "motif D peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys Met Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu
1 5 10 15

Thr Ile Asn Glu Glu Lys Thr Leu Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
 Saccharomyces cerevisiae cytochrome
 oxidase group II intron 1-encoded
 mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Glu Thr Pro Ala Arg Phe Leu Gly Tyr Asn Ile
 1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
 Drosophila melanogaster TART non-LTR
 retrotransposable element reverse
 transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ser Ile Leu Arg Ile Gly Tyr Tyr Pro Asp Ala Trp Lys His Ala Gln
 1 5 10 15

Val Lys Met Ile Leu Lys Pro Gly Lys Ser
 20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..29
(D) OTHER INFORMATION: /note= "motif 2 peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Arg Pro Ile Ser Leu Leu Ser Gly Leu Ser Lys Met Phe Glu Arg
1 5 10 15

Leu Leu Leu Lys Arg Leu Phe Arg Val Asp Leu Phe Lys
20 25

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..34
(D) OTHER INFORMATION: /note= "motif A peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Arg Lys Glu Tyr Cys Ser Ala Val Phe Leu Asp Ile Ser Glu Ala Phe
1 5 10 15

Asp Arg Val Trp His Glu Gly Leu Leu Leu Lys Leu Ala Lys Ile Leu
20 25 30

Pro Tyr

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

Arg Ala Gly Gln Ile Gly Ala Gly Val Pro Gln Gly Ser Asn Leu Gly
1           5           10           15
Pro Ile Leu Tyr Ser Ile Phe Ser Ser Asp Met Pro Leu Pro His Ile
          20           25           30
Tyr His Pro
          35

```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "motif C peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

Leu Ser Thr Tyr Ala Asp Asp Thr Ile Val Leu Ser Ser Asp Ile Leu
1           5           10           15
Ala

```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif D peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asn	Glu	Asn	Tyr	Leu	Lys	Thr	Phe	Ser	Asp	Trp	Ala	Asp	Lys	Trp	Gly
1					5				10					15	
Ile	Ser	Val	Asn	Ala	Ala	Lys	Thr	Gly	His						
			20				25								

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Glu	Ser	Lys	Gln	Ser	Tyr	Leu	Gly	Val	Ile	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 1 peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro
1				5				10						15	
Val	Phe	Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr						
			20				25								

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /note= "motif 2 and A peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp
1				5				10						15	
Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys
			20				25						30		
Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val
		35				40					45				
Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	
	50					55					60				

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Peptide

- (D) OTHER INFORMATION: /note= "motif B' peptide from HIV-1 reverse transcriptase"

Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser
1 5 10 15

Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Lys
20 25 30

Lys Gln Asn
35

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: Peptide

- (D) OTHER INFORMATION: /note= "motif C peptide from HIV-1 reverse transcriptase"

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..37
- (D) OTHER INFORMATION: /note= "motif D and E peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
1           5           10           15

Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
          20           25           30

Met Gly Ile Thr Leu
          35

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT finger sequence from motif 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Ile Pro Lys Lys
1

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..5

(D) OTHER INFORMATION: /note= "consensus telomerase RT palm,
primer grip sequence from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Leu Leu Arg Leu
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..4

(D) OTHER INFORMATION: /note= "consensus telomerase RT palm,
primer grip sequence from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Phe Leu
1

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: /note= "telomerase specific motif T
peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr
 1 5 10 15
 Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys
 20 25 30
 Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T'
 peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Glu Ala Glu Val Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif
 1 and 2 peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr
 1 5 10 15
 Ile

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B' peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu
 1 5 10 15
 Leu Cys Ser Leu Cys Tyr
 20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..13

(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr
1				5							10	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif D peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val
1					5					10				15	

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..11

(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from human TRT"

Glu Asn Asn Val Arg
1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif
1 and 2 peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys	Asn	Thr	Phe	Arg	Leu	Ile	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Arg	Lys	Lys	Tyr	Phe	Val	Arg	Ile	Asp	Ile	Lys	Ser	Cys	Tyr	Asp	Arg
1				5				10						15	

Ile

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B'
peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
 1 5 10 15
 Leu Cys His Phe Tyr Met
 20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip
motif C peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip
motif D peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly	Phe	Glu	Lys	His	Asn	Phe	Ser	Thr	Ser	Leu	Glu	Lys	Thr	Val	Ile
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from Schizosaccharomyces pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Phe	Phe	Gly	Phe	Ser	Val	Asn	Met	Arg	Ser	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "telomerase specific motif T peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Trp	Ile	Phe	Glu	Asp	Leu	Val	Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr
1				5					10					15	

Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys
			20					25					30		

Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser	Ile
			35				40			

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T'
peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Glu Lys Glu Val Glu
1 5

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif
1 and 2 peptide from Euplotes
aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser
 1 5 10 15
 Val

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B' peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
 1 5 10 15
 Leu Ser Ser Phe Tyr Tyr
 20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif D peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Trp Ile Gly Ile Ser Ile Asp Met Lys Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "telomerase specific motif T
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1           5           10           15
Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
          20           25           30
Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile
          35           40

```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T'
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

Glu Asn Asn Val Cys
1           5

```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..11
(D) OTHER INFORMATION: /note= "telomerase RT finger motif 1
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..5
(D) OTHER INFORMATION: /note= "telomerase RT finger motif 2
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe Arg Ile Ile Ala
1 5

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser
 1 5 10 15
 Ile

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B' peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro
 1 5 10 15
 Ile Val Asp Leu Val Tyr
 20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu	Ile	Leu	Lys	Leu	Ala	Asp	Asp	Phe	Leu	Ile	Ile	Ser
1				5					10			

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif D peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gly	Phe	Gln	Lys	Tyr	Asn	Ala	Lys	Ala	Asn	Arg	Asp	Lys	Ile	Leu	Ala
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp	Lys	His	Ser	Ser	Thr	Met	Asn	Asn	Phe	His
1				5					10	

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /note= "NFkappaB CS1 binding site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGGRHTYYHC

10

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "NFkappaB MHC I.2 binding site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGGGCTTCCC C

11

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "NFkappaB CS2 binding site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

RGGGRMTYYC C

11

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "topoisomerase II cleavage site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

RNYNNCNGY NGKTNINY

18

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 101..3196
- (D) OTHER INFORMATION: /note= "Euplotes aediculatus 123 kDa telomerase protein subunit (TRT)"
/codon= (seq: "tga", aa: Cys)
/product= "Euplotes aediculatus 123 kDa telomerase protein subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AAAACCCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA 60

TTAATAAGCT CAGATTTTAA ATATTAATTA CAAACCTAA ATG GAG GTT GAT GTT 115
Met Glu Val Asp Val
1 5

GAT AAT CAA GCT GAT AAT CAT GGC ATT CAC TCA GCT CTT AAG ACT TGT 163
Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala Leu Lys Thr Cys
10 15 20

GAA GAA ATT AAA GAA GCT AAA ACG TTG TAC TCT TGG ATC CAG AAA GTT Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp Ile Gln Lys Val 25 30 35	211
ATT AGA TGA AGA AAT CAA TCT CAA AGT CAT TAT AAA GAT TTA GAA GAT Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys Asp Leu Glu Asp 40 45 50	259
ATT AAA ATA TTT GCG CAG ACA AAT ATT GTT GCT ACT CCA CGA GAC TAT Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr Pro Arg Asp Tyr 55 60 65	307
AAT GAA GAA GAT TTT AAA GTT ATT GCA AGA AAA GAA GTA TTT TCA ACT Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu Val Phe Ser Thr 70 75 80 85	355
GGA CTA ATG ATC GAA CTT ATT GAC AAA TGC TTA GTT GAA CTT CTT TCA Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val Glu Leu Leu Ser 90 95 100	403
TCA AGC GAT GTT TCA GAT AGA CAA AAA CTT CAA TGA TTT GGA TTT CAA Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys Phe Gly Phe Gln 105 110 115	451
CTT AAG GGA AAT CAA TTA GCA AAG ACC CAT TTA TTA ACA GCT CTT TCA Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu Thr Ala Leu Ser 120 125 130	499
ACT CAA AAG CAG TAT TTC TTT CAA GAC GAA TGG AAC CAA GTT AGA GCA Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn Gln Val Arg Ala 135 140 145	547
ATG ATT GGA AAT GAG CTC TTC CGA CAT CTC TAC ACT AAA TAT TTA ATA Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr Lys Tyr Leu Ile 150 155 160 165	595
TTC CAG CGA ACT TCT GAA GGA ACT CTT GTT CAA TTT TGC GGG AAT AAC Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe Cys Gly Asn Asn 170 175 180	643
GTT TTT GAT CAT TTG AAA GTC AAC GAT AAG TTT GAC AAA AAG CAA AAA Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp Lys Lys Gln Lys 185 190 195	691
GGT GGA GCA GCA GAC ATG AAT GAA CCT CGA TGT TGA TCA ACC TGC AAA Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys Ser Thr Cys Lys 200 205 210	739
TAC AAT GTC AAG AAT GAG AAA GAT CAC TTT CTC AAC AAC ATC AAC GTG Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn Asn Ile Asn Val 215 220 225	787
CCG AAT TGG AAT AAT ATG AAA TCA AGA ACC AGA ATA TTT TAT TGC ACT Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile Phe Tyr Cys Thr 230 235 240 245	835
CAT TTT AAT AGA AAT AAC CAA TTC TTC AAA AAG CAT GAG TTT GTG AGT His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His Glu Phe Val Ser 250 255 260	883

AAC AAA AAC AAT ATT TCA GCG ATG GAC AGA GCT CAG ACG ATA TTC ACG	931
Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln Thr Ile Phe Thr	
265 270 275	
AAT ATA TTC AGA TTT AAT AGA ATT AGA AAG AAG CTA AAA GAT AAG GTT	979
Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu Lys Asp Lys Val	
280 285 290	
ATC GAA AAA ATT GCC TAC ATG CTT GAG AAA GTC AAA GAT TTT AAC TTC	1027
Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys Asp Phe Asn Phe	
295 300 305	
AAC TAC TAT TTA ACA AAA TCT TGT CCT CTT CCA GAA AAT TGG CGG GAA	1075
Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu Asn Trp Arg Glu	
310 315 320 325	
CGG AAA CAA AAA ATC GAA AAC TTG ATA AAT AAA ACT AGA GAA GAA AAG	1123
Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr Arg Glu Glu Lys	
330 335 340	
TCG AAG TAC TAT GAA GAG CTG TTT AGC TAC ACA ACT GAT AAT AAA TGC	1171
Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr Asp Asn Lys Cys	
345 350 355	
GTC ACA CAA TTT ATT AAT GAA TTT TTC TAC AAT ATA CTC CCC AAA GAC	1219
Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile Leu Pro Lys Asp	
360 365 370	
TTT TTG ACT GGA AGA AAC CGT AAG AAT TTT CAA AAG AAA GTT AAG AAA	1267
Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys Lys Val Lys Lys	
375 380 385	
TAT GTG GAA CTA AAC AAG CAT GAA CTC ATT CAC AAA AAC TTA TTG CTT	1315
Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys Asn Leu Leu Leu	
390 395 400 405	
GAG AAG ATC AAT ACA AGA GAA ATA TCA TGG ATG CAG GTT GAG ACC TCT	1363
Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser	
410 415 420	
GCA AAG CAT TTT TAT TAT TTT GAT CAC GAA AAC ATC TAC GTC TTA TGG	1411
Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp	
425 430 435	
AAA TTG CTC CGA TGG ATA TTC GAG GAT CTC GTC GTC TCG CTG ATT AGA	1459
Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg	
440 445 450	
TGA TTT TTC TAT GTC ACC GAG CAA CAG AAA AGT TAC TCC AAA ACC TAT	1507
Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr	
455 460 465	
TAC TAC AGA AAG AAT ATT TGG GAC GTC ATT ATG AAA ATG TCA ATC GCA	1555
Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala	
470 475 480 485	
GAC TTA AAG AAG GAA ACG CTT GCT GAG GTC CAA GAA AAA GAG GTT GAA	1603
Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu	
490 495 500	

GAA TGG AAA AAG TCG CTT GGA TTT GCA CCT GGA AAA CTC AGA CTA ATA Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile 505 510 515	1651
CCG AAG AAA ACT ACT TTC CGT CCA ATT ATG ACT TTC AAT AAG AAG ATT Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile 520 525 530	1699
GTA AAT TCA GAC CGG AAG ACT ACA AAA TTA ACT ACA AAT ACG AAG TTA Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu 535 540 545	1747
TTG AAC TCT CAC TTA ATG CTT AAG ACA TTG AAG AAT AGA ATG TTT AAA Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys 550 555 560 565	1795
GAT CCT TTT GGA TTC GCT GTT TTT AAC TAT GAT GAT GTA ATG AAA AAG Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys 570 575 580	1843
TAT GAG GAG TTT GTT TGC AAA TGG AAG CAA GTT GGA CAA CCA AAA CTC Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu 585 590 595	1891
TTC TTT GCA ACT ATG GAT ATC GAA AAG TGA TAT GAT AGT GTA AAC AGA Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg 600 605 610	1939
GAA AAA CTA TCA ACA TTC CTA AAA ACT ACT AAA TTA CTT TCT TCA GAT Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp 615 620 625	1987
TTC TGG ATT ATG ACT GCA CAA ATT CTA AAG AGA AAG AAT AAC ATA GTT Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn Ile Val 630 635 640 645	2035
ATC GAT TCG AAA AAC TTT AGA AAG AAA GAA ATG AAA GAT TAT TTT AGA Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr Phe Arg 650 655 660	2083
CAG AAA TTC CAG AAG ATT GCA CTT GAA GGA GGA CAA TAT CCA ACC TTA Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro Thr Leu 665 670 675	2131
TTC AGT GTT CTT GAA AAT GAA CAA AAT GAC TTA AAT GCA AAG AAA ACA Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys Lys Thr 680 685 690	2179
TTA ATT GTT GAA GCA AAG CAA AGA AAT TAT TTT AAG AAA GAT AAC TTA Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp Asn Leu 695 700 705	2227
CTT CAA CCA GTC ATT AAT ATT TGC CAA TAT AAT TAC ATT AAC TTT AAT Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn Phe Asn 710 715 720 725	2275
GGG AAG TTT TAT AAA CAA ACA AAA GGA ATT CCT CAA GGT CTT TGA GTT Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val 730 735 740	2323

TCA TCA ATT TTG TCA TCA TTT TAT TAT GCA ACA TTA GAG GAA AGC TCC Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser 745 750 755	2371
TTA GGA TTC CTT AGA GAT GAA TCA ATG AAC CCT GAA AAT CCA AAT GTT Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro Asn Val 760 765 770	2419
AAT CTT CTA ATG AGA CTT ACA GAT GAC TAT CTT TTG ATT ACA ACT CAA Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln 775 780 785	2467
GAG AAT AAT GCA GTA TTG TTT ATT GAG AAA CTT ATA AAC GTA AGT CGT Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg 790 795 800 805	2515
GAA AAT GGA TTT AAA TTC AAT ATG AAG AAA CTA CAG ACT AGT TTT CCA Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro 810 815 820	2563
TTA AGT CCA AGC AAA TTT GCA AAA TAC GGA ATG GAT AGT GTT GAG GAG Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val Glu Glu 825 830 835	2611
CAA AAT ATT GTT CAA GAT TAC TGC GAT TGG ATT GGC ATC TCA ATT GAT Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile Asp 840 845 850	2659
ATG AAA ACT CTT GCT TTA ATG CCA AAT ATT AAC TTG AGA ATA GAA GGA Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile Glu Gly 855 860 865	2707
ATT CTG TGT ACA CTC AAT CTA AAC ATG CAA ACA AAG AAA GCA TCA ATG Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala Ser Met 870 875 880 885	2755
TGG CTC AAG AAG AAA CTA AAG TCG TTT TTA ATG AAT AAC ATT ACC CAT Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile Thr His 890 895 900	2803
TAT TTT AGA AAG ACG ATT ACA ACC GAA GAC TTT GCG AAT AAA ACT CTC Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys Thr Leu 905 910 915	2851
AAC AAG TTA TTT ATA TCA GGC GGT TAC AAA TAC ATG CAA TGA GCC AAA Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys Ala Lys 920 925 930	2899
GAA TAC AAG GAC CAC TTT AAG AAG AAC TTA GCT ATG AGC AGT ATG ATC Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser Met Ile 935 940 945	2947
GAC TTA GAG GTA TCT AAA ATT ATA TAC TCT GTA ACC AGA GCA TTC TTT Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala Phe Phe 950 955 960 965	2995
AAA TAC CTT GTG TGC AAT ATT AAG GAT ACA ATT TTT GGA GAG GAG CAT Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu Glu His 970 975 980	3043

TAT CCA GAC TTT TTC CTT AGC ACA CTG AAG CAC TTT ATT GAA ATA TTC 3091
 Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu Ile Phe
 985 990 995

AGC ACA AAA AAG TAC ATT TTC AAC AGA GTT TGC ATG ATC CTC AAG GCA 3139
 Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu Lys Ala
 1000 1005 1010

AAA GAA GCA AAG CTA AAA AGT GAC CAA TGT CAA TCT CTA ATT CAA TAT 3187
 Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile Gln Tyr
 1015 1020 1025

GAT GCA TAGTCGACTA TTCTAACTTA TTTTGGAAAG TTAATTTTCA ATTTTGTCT 3243
 Asp Ala
 1030

TATATACTGG GGTTTTGGGG TTTTGGGGTT TTGGGG 3279

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
 1 5 10 15

Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
 20 25 30

Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
 35 40 45

Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
 50 55 60

Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
 65 70 75 80

Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
 85 90 95

Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
 100 105 110

Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
 115 120 125

Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
 130 135 140

Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
 145 150 155 160

Thr	Lys	Tyr	Leu	Ile	Phe	Gln	Arg	Thr	Ser	Glu	Gly	Thr	Leu	Val	Gln		
				165					170						175		
Phe	Cys	Gly	Asn	Asn	Val	Phe	Asp	His	Leu	Lys	Val	Asn	Asp	Lys	Phe		
			180					185					190				
Asp	Lys	Lys	Gln	Lys	Gly	Gly	Ala	Ala	Asp	Met	Asn	Glu	Pro	Arg	Cys		
		195					200					205					
Cys	Ser	Thr	Cys	Lys	Tyr	Asn	Val	Lys	Asn	Glu	Lys	Asp	His	Phe	Leu		
	210					215					220						
Asn	Asn	Ile	Asn	Val	Pro	Asn	Trp	Asn	Asn	Met	Lys	Ser	Arg	Thr	Arg		
225				230						235					240		
Ile	Phe	Tyr	Cys	Thr	His	Phe	Asn	Arg	Asn	Asn	Gln	Phe	Phe	Lys	Lys		
				245					250						255		
His	Glu	Phe	Val	Ser	Asn	Lys	Asn	Asn	Ile	Ser	Ala	Met	Asp	Arg	Ala		
			260					265					270				
Gln	Thr	Ile	Phe	Thr	Asn	Ile	Phe	Arg	Phe	Asn	Arg	Ile	Arg	Lys	Lys		
		275					280						285				
Leu	Lys	Asp	Lys	Val	Ile	Glu	Lys	Ile	Ala	Tyr	Met	Leu	Glu	Lys	Val		
	290					295					300						
Lys	Asp	Phe	Asn	Phe	Asn	Tyr	Tyr	Leu	Thr	Lys	Ser	Cys	Pro	Leu	Pro		
305					310					315					320		
Glu	Asn	Trp	Arg	Glu	Arg	Lys	Gln	Lys	Ile	Glu	Asn	Leu	Ile	Asn	Lys		
				325					330					335			
Thr	Arg	Glu	Glu	Lys	Ser	Lys	Tyr	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Thr		
			340					345						350			
Thr	Asp	Asn	Lys	Cys	Val	Thr	Gln	Phe	Ile	Asn	Glu	Phe	Phe	Tyr	Asn		
		355					360					365					
Ile	Leu	Pro	Lys	Asp	Phe	Leu	Thr	Gly	Arg	Asn	Arg	Lys	Asn	Phe	Gln		
	370					375					380						
Lys	Lys	Val	Lys	Lys	Tyr	Val	Glu	Leu	Asn	Lys	His	Glu	Leu	Ile	His		
385					390					395					400		
Lys	Asn	Leu	Leu	Leu	Glu	Lys	Ile	Asn	Thr	Arg	Glu	Ile	Ser	Trp	Met		
				405					410					415			
Gln	Val	Glu	Thr	Ser	Ala	Lys	His	Phe	Tyr	Tyr	Phe	Asp	His	Glu	Asn		
			420					425					430				
Ile	Tyr	Val	Leu	Trp	Lys	Leu	Leu	Arg	Trp	Ile	Phe	Glu	Asp	Leu	Val		
		435					440					445					
Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln	Lys	Ser		
	450					455					460						
Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met		
465					470					475					480		

Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
 485 490 495
 Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
 500 505 510
 Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
 515 520 525
 Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
 530 535 540
 Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
 545 550 555 560
 Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
 565 570 575
 Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
 580 585 590
 Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 595 600 605
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 610 615 620
 Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
 625 630 635 640
 Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
 645 650 655
 Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
 660 665 670
 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
 675 680 685
 Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
 690 695 700
 Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
 705 710 715 720
 Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
 725 730 735
 Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
 740 745 750
 Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
 755 760 765
 Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
 770 775 780
 Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
 785 790 795 800

Ile	Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu
				805					810					815	
Gln	Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met
			820					825					830		
Asp	Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile
		835					840					845			
Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn
	850					855					860				
Leu	Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr
865					870					875					880
Lys	Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met
				885					890					895	
Asn	Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe
			900					905					910		
Ala	Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr
		915					920					925			
Met	Gln	Cys	Ala	Lys	Glu	Tyr	Lys	Asp	His	Phe	Lys	Lys	Asn	Leu	Ala
	930					935					940				
Met	Ser	Ser	Met	Ile	Asp	Leu	Glu	Val	Ser	Lys	Ile	Ile	Tyr	Ser	Val
945					950					955					960
Thr	Arg	Ala	Phe	Phe	Lys	Tyr	Leu	Val	Cys	Asn	Ile	Lys	Asp	Thr	Ile
				965					970					975	
Phe	Gly	Glu	Glu	His	Tyr	Pro	Asp	Phe	Phe	Leu	Ser	Thr	Leu	Lys	His
			980					985					990		
Phe	Ile	Glu	Ile	Phe	Ser	Thr	Lys	Lys	Tyr	Ile	Phe	Asn	Arg	Val	Cys
		995					1000					1005			
Met	Ile	Leu	Lys	Ala	Lys	Glu	Ala	Lys	Leu	Lys	Ser	Asp	Gln	Cys	Gln
	1010					1015					1020				
Ser	Leu	Ile	Gln	Tyr	Asp	Ala									
1025					1030										

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(959..1216, 1273..1353, 1425..1543,
1595..1857, 1894..2286, 2326..2396, 2436..2705,
2746..2862, 2914..3083, 3125..3309, 3356..3504,
3546..3759, 3797..4046, 4086..4252, 4296..4392,
4435..4597)(D) OTHER INFORMATION: /note= "Schizosaccharomyces pombe
telomerase catalytic subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GGTACCGATT TACTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACTTCC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTTCG	240
GGTTCGCTTA CTTTAAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTT	300
TCTACCCCGT CATTGGATAT AGCTCTTGGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCGCGAAA GTTTTTTGAT	540
GCTTGACACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT	600
AACGCGGTTT TATTTTTCTA TTTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TTCACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780
TGTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA	840
AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAAACGTTA	900
TGATCAGTAG GACACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC	958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG	1006
Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu	
1 5 10 15	
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT	1054
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val	
20 25 30	
TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG	1102
Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu	
35 40 45	
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA	1150
Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val	
50 55 60	

GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro 65 70 75 80	1198
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGT TTTTG ATTTTTTCT Lys Cys Ser Gln Ser Glu 85	1246
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG Leu Ile Ala Asn Val Val Lys Gln Met 90 95	1299
TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe 100 105 110	1347
TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTTCAAAGA Ser Met	1403
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA Asn His Glu Asp Phe Arg Ala Met His Val 115 120	1454
ACC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile 125 130 135	1502
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Leu Glu Ile 140 145 150	1543
GTAAATACCG GTTAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC Ile	1598
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu 155 160 165 170	1646
GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTAAC TAATA CTGTTATCCT TCATAACTAA Tyr Lys Lys Phe Lys Gln 235 240	1887

TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030
CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile 290 295 300	2078
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr 305 310 315	2126
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu 320 325 330	2174
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile 335 340 345 350	2222
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe 355 360 365	2270
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC 2327 Glu Ile Ile Leu Lys 370	Asp
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His 375 380 385	2375
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTTT ACCATTAATT Tyr Leu Met Ser Asn Ile Lys 390 395	2426
AACAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser 400 405	2474
AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe 410 415 420	2522
GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu 425 430 435 440	2570
CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr 445 450 455	2618

GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile 460 465 470	2666
ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu 475 480 485	2715
GTATTTTTTTG CAAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG Asn Asn Val Arg Met Asp Thr Gln 490	2769
AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn 495 500 505	2817
ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys 510 515 520	2862
GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT Met Gly 525	2919
TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val 530 535 540	2967
GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro 545 550 555	3015
TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu 560 565 570	3063
CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT Leu Lys His Arg Met Phe Gly 575 580	3113
TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser 585 590	3161
TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys 595 600 605	3209
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His 610 615 620 625	3257
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser 630 635 640	3305
TAT T GTAAGTTTAT TTTTTCATTG GAATTTTTTA ACAAATTCTT TTTTAG TT Tyr Phe	3357

GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr 645 650 655	3405
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser 660 665 670 675	3453
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val 680 685 690	3501
AAG GTATACCAAT TGTGGAATTG TAATAACACT AATGAAACTA G ATA GGA AAT Lys Ile Gly Asn 695	3554
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser 700 705 710	3602
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu 715 720 725	3650
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp 730 735 740	3698
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn 745 750 755	3746
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA Leu Ser Leu Arg Gly 760	3798
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn 765 770 775 780	3846
TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795	3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu 800 805 810	3942
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser 815 820 825	3990
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys 830 835 840	4038
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG Ile Leu Arg Ser 845	4089

AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser 850 855 860	4137
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys 865 870 875 880	4185
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro 885 890 895	4233
CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT Gln Arg Met Phe Ile Thr 900	4282
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys 905 910	4330
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser 915 920 925 930	4378
GCA GAA GTC AAA TG GTACGTGTCG GTCTCGAGAC TTCAGCAATA TTGACACATC Ala Glu Val Lys Trp 935	4432
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys 940 945 950	4480
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr 955 960 965	4528
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu 970 975 980	4576
CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC His Arg Arg Ile Ala Asp 985	4624
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC	4684
ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC	4744
TTTATCCTTA TACTTTTAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCCCA	4804
TTAAACGGGA GTGGTTAAAC ATTAAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA	4864
ATAAGGAAAG TGGTTTTCTA TAATGAATAA TGCCCCGCACT AATGCAAAAA GACGAAGATT	4924
ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT	4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG	5044
TGACCGAATT TTGGTAAAAG CCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG	5104
AAAAGAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTTT	5164

GTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA 5224
 TTCCGAAATA GCCAAATTTT TGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC 5284
 TTATGAGGCT TCAAAAACCTC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT 5344
 GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTG CAAAAAAGAA AATATCATTG 5404
 GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT 5464
 AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA 5524
 GTTAAGTGAC CAAAGGTACC 5544

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu
 1 5 10 15
 Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val
 20 25 30
 Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu
 35 40 45
 Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val
 50 55 60
 Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro
 65 70 75 80
 Lys Cys Ser Gln Ser Glu Leu Ile Ala Asn Val Val Lys Gln Met Phe
 85 90 95
 Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe Ser
 100 105 110
 Met Asn His Glu Asp Phe Arg Ala Met His Val Asn Gly Val Gln Asn
 115 120 125
 Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile Ser Ile Leu Glu Ser
 130 135 140
 Lys Asn Trp Gln Leu Leu Leu Glu Ile Ile Gly Ser Asp Ala Met His
 145 150 155 160
 Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu Ala Leu Pro Asn Asp Asn
 165 170 175
 Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe Lys Asn Asn Val Phe Glu
 180 185 190

Glu Thr Val Ser Lys Lys Arg Lys Arg Thr Ile Glu Thr Ser Ile Thr
 195 200 205
 Gln Asn Lys Ser Ala Arg Lys Glu Val Ser Trp Asn Ser Ile Ser Ile
 210 215 220
 Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser Tyr Lys Lys Phe Lys Gln
 225 230 235 240
 Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr Val His
 245 250 255
 Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile Asn Ala
 260 265 270
 Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser Gln Ser
 275 280 285
 Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile Glu Gln
 290 295 300
 Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr Asn His
 305 310 315 320
 Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu Ser Tyr
 325 330 335
 Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile Leu Val
 340 345 350
 Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe Glu Ile
 355 360 365
 Ile Leu Lys Asp Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser
 370 375 380
 Phe Ser Leu His Tyr Leu Met Ser Asn Ile Lys Ile Ser Glu Ile Glu
 385 390 395 400
 Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys Met Cys Leu Ser Asp
 405 410 415
 Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe Ile Tyr Trp Leu Tyr
 420 425 430
 Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu
 435 440 445
 Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp
 450 455 460
 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe
 465 470 475 480
 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr
 485 490 495
 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg
 500 505 510

Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn
 515 520 525
 Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser
 530 535 540
 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn
 545 550 555 560
 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys
 565 570 575
 His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys
 580 585 590
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 595 600 605
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile
 610 615 620
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe
 625 630 635 640
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser
 645 650 655
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr
 660 665 670
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly
 675 680 685
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile
 690 695 700
 Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 705 710 715 720
 Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val
 725 730 735
 Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 740 745 750
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 755 760 765
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser
 770 775 780
 Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met
 785 790 795 800
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu
 805 810 815
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu
 820 825 830

Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser
 835 840 845
 Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser
 850 855 860
 Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys
 865 870 875 880
 Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro
 885 890 895
 Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile
 900 905 910
 Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu
 915 920 925
 Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly
 930 935 940
 Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr
 945 950 955 960
 Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu
 965 970 975
 Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp
 980 985

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GGGGTTTTGG GGTTTT

16

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1762
- (D) OTHER INFORMATION: /note= "gene encoding the 43 kDa telomerase protein subunit from *Euplotes aediculatus*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

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CCCCAAAACC CCAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG GTAGTTTAGA      60
AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT      120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTGTAG TGACAAGAAA GGATGCAAAA      180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG      240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA      300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA      360
TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA      420
TACTAAAAGG TAAACAGTTT GGATTATTTT CCTAGCCAAC AATGATGAGT ATATTAAATT      480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAGACA AACTCGCTAT      540
AAAACGCAAG AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTAATTTCG      600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT      660
TGAAAAAGCT GTTTACAAC TGAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT      720
TATTTTGTGA ATTAATCTCA AATATCTTAT CTCAATTTAA TGGATAGCTA TAGAAACAAA      780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC      840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC      900
TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT AAAAGAAGCA      960
GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAT TTGTTGATTC TTCTGTAACC     1020
GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTC     1080
TTAAAGATTT CAAAATTCC AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG     1140
TTTTTCATTT CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA     1200

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GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCAT 1260
 AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTTAAAAA 1320
 TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA 1380
 GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA 1440
 ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA 1500
 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA 1560
 TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT 1620
 ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA 1680
 GTACAGAAGT GAAGAAATAA AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT 1740
 TTGGGGTTTT GGGGTTTTGG GG 1762

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Pro Gln Asn Pro Lys Thr Pro Lys Pro Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Lys Lys Lys Lys Leu Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Arg Asn Lys Ile Leu Phe Pro His Lys Trp Arg Trp Ile Leu Ile
 1 5 10 15

Trp Met Ile .

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Lys Ile Tyr Phe Leu Ile His Ser Thr Ser Ile Ala Ala Leu Val Val
 1 5 10 15

Thr Arg Lys Asp Ala Lys His Cys Asn Leu Ala Arg Asn Arg Leu His
 20 25 30

Cys Leu Phe Gln Ser Cys Lys Asn Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ser Ser Thr Ser Arg Met Gln Ile Phe Ile Thr Ile Leu Ser Cys Glu
 1 5 10 15

Asn

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Lys Ala Glu Ser Lys Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Lys Leu Lys His Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Cys Leu Asn Lys Ile Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Cys Gly Leu Phe Tyr Phe Leu Asp His Phe Leu Arg Ser Ile Met Glu
1 5 10 15

Lys Ile Thr

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Lys Val Asn Ser Leu Asp Tyr Phe Pro Ser Gln Gln Cys Cys Val Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Ile His Met Arg Met Ser Gln Arg Ile Ser Ile His Gln Thr Tyr Gln
1 5 10 15

Arg Gln Thr Arg Tyr Lys Thr Gln Glu Lys Val Cys
20 25

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ser Asn Ser Arg Arg Thr Tyr Cys Ile Tyr Tyr Ser Tyr Gly Phe Tyr
1 5 10 15

Tyr Asn Cys Phe Arg Tyr Arg Arg Cys Thr Pro Glu Ser Cys Asp Asn
 20 25 30

Cys Lys Ser Cys Leu Gln Leu Lys Glu Ser Gln Phe Cys Lys Phe Cys
 35 40 45

Cys Val Cys His Tyr Phe Val Asn
 50 55

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Ser Gln Ile Ser Tyr Leu Asn Leu Met Asp Ser Tyr Arg Asn Lys Pro
 1 5 10 15

Asn Lys Pro Cys Lys Phe Asn Gly Ile Tyr Val Lys Ser Phe Gly Thr
 20 25 30

Asn Ala His Cys Ile Tyr Ile Gly Phe Leu Lys His Arg Tyr Thr Glu
 35 40 45

Cys Phe Arg Asp Cys Phe Ser Leu Gln Gln Ile Thr Cys Phe Asp Tyr
 50 55 60

Ser Cys Ser Ser Leu Ile Ser Leu Lys Glu Ala Gly Glu Met Lys Arg
 65 70 75 80

Arg Leu Lys Lys Glu Ile Ser Lys Phe Val Asp Ser Ser Val Thr Gly
 85 90 95

Ile Asn Asn Lys Asn Ile Ser Asn Glu Lys Glu Glu Glu Leu Ser Gln
 100 105 110

Ser Cys Phe Leu Lys Ile Ser Lys Ile Pro Gly Lys Arg Asp Thr Phe
 115 120 125

Ile Lys Ile His Ile Leu
 130

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Phe	Phe	Ile	Ser	Gln	Leu	Leu	Phe	Ser	Phe	Ile	Leu	Thr	Ile	Phe	Phe
1				5				10						15	

Asp

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Leu	Glu	Val	Lys	Ser	Ile	Lys
1			5			

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Thr	Glu	Val	Thr
1			

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Leu	Ile	His	Ile	His	Arg	Ser	Thr	Phe	Ile	Tyr	Pro	Ile	Arg	Cys
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Gly Asn Ser Ser His Pro Phe
1 5

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Cys Tyr Glu Asp
1

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ile Phe Arg Val Lys Lys Trp Ser Arg Asn Leu Asn Gln Lys Glu Leu
1 5 10 15
Arg Arg Tyr Cys Lys Arg Ile Glu Leu
20 25

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Val Leu Pro Ile Leu Ile Asp Cys Arg Asp Cys Arg Gly Asn Cys Thr
1 5 10 15

Glu Asp His

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Arg Asn Lys Val Thr Phe Ile Asn
1 5

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ile Thr Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Thr Ile Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly Lys Glu
1 5 10 15

Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln
 20 25

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Lys Cys Val Gln Lys Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn
 1 5 10 15

Asn Leu Leu Lys Arg Gly Val Leu Gly Phe Trp Gly Phe Gly
 20 25 30

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Pro Lys Thr Pro Lys Pro Gln Asn Pro Tyr Lys Lys Arg Lys Asn Cys
 1 5 10 15

Gly Ser Leu Glu Ile Lys Tyr Tyr Ser Arg Thr Asn Gly Asp Gly Tyr
 20 25 30

Cys Phe Gly Cys Tyr Arg Lys Phe Thr Ser
 35 40

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Tyr Ile Gln Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Cys Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala Phe
1 5 10 15

Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu Gly
20 25 30

Cys Lys Ser Leu
35

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys Arg Arg Ala Lys Ser
1 5 10 15

Arg Asn Cys Asn Ile Thr Asn Val
20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Ile Lys Ser Gly Asn Glu Asp Tyr Ser Ile Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gly Ala Leu Trp Arg Lys Leu Leu Asn Thr Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Thr Val Trp Ile Ile Ser Leu Ala Asn Asn Asp Glu Tyr Ile Lys Phe
1 5 10 15

Ile Cys Glu Cys Val Lys Gly Ser Arg Tyr Ile Arg Leu Thr Lys Asp
20 25 30

Lys Leu Ala Ile Lys Arg Lys Lys Lys Phe Asp Asn Arg Thr Ala Glu
35 40 45

Glu Leu Ile Ala Phe Thr Ile Arg Met Gly Phe Ile Thr Ile Val Leu
50 55 60

Gly Ile Asp Gly Glu Leu Pro Ser Leu Glu Thr Ile Glu Lys Ala Val
65 70 75 80

Tyr Asn Cys Arg Asn Arg Ser Ser Glu Ser Ser Asp Val Tyr Ala Ile
85 90 95

Ile Leu Cys Ile Asn Leu Lys Tyr Leu Ile Ser Ile
100 105

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser Leu Met Glu
 1 5 10 15

Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe Ile Leu Asp
 20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu Ala Tyr Asn Arg
 1 5 10 15

Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Lys Lys Gln Ala Lys Cys Lys Glu Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Arg Lys Arg Phe Gln Asn Leu Leu Ile Leu Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys Lys Lys Lys Ser Tyr
 1 5 10 15

His Asn Pro Asp Ser
 20

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Arg Phe Gln Lys Phe Gln Val Arg Glu Ile His Ser Leu Lys Phe Ile
 1 5 10 15

Tyr Tyr Ser Phe Ser Phe His Ser Cys Tyr Phe Leu Leu Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Gln Tyr Phe Leu Ile Ser Trp Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Leu Ser Leu Phe Thr Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp
 1 5 10 15

Asp Lys Glu Thr Ala Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr
 20 25 30

Lys Phe Leu Glu Ser Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn
 35 40 45

Cys Val Asp Ile Ala Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys
 50 55 60

Tyr Tyr Gln Ser Cys Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln
 65 70 75 80

Lys Ile Ile Lys Glu Ile Lys
85

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Leu Leu Leu Ile Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Thr Lys Leu Leu Ile
1 5

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Arg Ser Ala Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg
1 5 10 15

Gln

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Lys Ile Gln Thr Leu Val Lys Ile Leu Arg Lys Glu Lys Lys Thr Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Gln Lys Lys Lys
 1

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Tyr Arg Ser Glu Glu Ile Lys Asp Leu Phe Phe Ser Ile Ile
 1 5 10 15

Tyr Cys Lys Glu Gly Phe Trp Gly Phe Gly Val Leu Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Pro Lys Pro Gln Asn Pro Lys Thr Pro Ile Lys Lys Glu Lys Ile Glu
1 5 10 15
Val Val

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile Asp Leu Asp Asp Ile
1 5 10 15
Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser
20 25 30
Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser
35 40 45
Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp
50 55 60
Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser
65 70 75 80
Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu Met Phe Lys
85 90

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser Leu Leu Lys Glu
1 5 10 15

His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys Gln Phe Gly Leu
 20 25 30

Phe Pro

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Pro Thr Met Met Ser Ile Leu Asn Ser Tyr Glu Asn Glu Ser Lys Asp
 1 5 10 15

Leu Asp Thr Ser Asp Leu Pro Lys Thr Asn Ser Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Asn Ala Arg Lys Ser Leu Ile Ile Glu Gln Gln Lys Asn Leu Leu His
 1 5 10 15

Leu Leu Phe Val Trp Val Leu Leu Gln Leu Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Val Ser Thr Val Asn Ser Arg Val Leu Arg Gln Leu Lys Lys Leu Phe
 1 5 10 15

Thr	Thr	Glu	Gly	Ile	Ala	Val	Leu	Lys	Val	Leu	Met	Cys	Met	Pro	Leu
			20					25					30		
Phe	Cys	Glu	Leu	Ile	Ser	Asn	Ile	Leu	Ser	Gln	Phe	Asn	Gly		
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Lys Gln Thr Lys
1

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Thr Met Gln Val
1

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Trp Asn Ile Arg
1

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Ile Leu Trp Asp Lys Cys Thr Leu Asn Leu Tyr Trp Ile Leu Lys Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Ile His Arg Met Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Leu Thr Thr Asp Tyr Leu Phe Cys Leu Leu Leu Ile Ser Tyr Ile
 1 5 10 15

Phe Lys Arg Ser Arg Arg Asn Glu Lys Lys Thr Lys Glu Arg Asp Phe
 20 25 30

Lys Ile Cys Cys Phe Phe Cys Asn Arg Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Gln Gln Glu Tyr
1

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Gln Arg Lys Arg Arg Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe
1 5 10 15

Lys Asn Ser Arg
 20

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Glu Arg Tyr Ile His
1 5

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Asn Ser Tyr Ile Ile Val Phe His Phe Thr Ala Val Ile Phe Phe Tyr
1           5           10           15
Leu Asn Asn Ile Phe Cys Leu Ala Gly Ser Lys Lys Tyr Gln Ile Arg
          20           25           30
Glu Ala Leu Asp Cys Gly Asn Leu Ala Tyr Ser His Ser
          35           40           45

```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

Ile Asp Leu His Ile Ser Asn Thr Met Ile Arg Lys Gln Gln Ser Ser
1           5           10           15
Val Leu Lys Ile Val Leu Cys Gly Leu Asn Phe
          20           25

```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

Ser Gln Glu Met Glu Pro Lys Ser
1           5

```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg Thr Leu Asn Leu
 1 5 10 15
 Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys Arg Leu Thr Arg
 20 25 30
 Gln Leu His Arg Arg Ser Leu Lys Lys
 35 40

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Ser Asn Phe Tyr
 1

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Leu Glu Asn Lys Leu Asn Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Tyr Arg Asp Gln Arg Ser Ser Ile Asp Glu Ile Lys Ala Glu Leu Lys
 1 5 10 15

Leu Asp Asn Lys Lys Tyr Lys Pro Trp Ser Lys Tyr Cys Gly Arg Lys
 20 25 30

Arg Arg Pro Val Ser Lys Arg Lys Asn Lys Ala Ile Asn Lys Met Ser
 35 40 45

Thr Glu Val Lys Lys
 50

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Lys Ile Tyr Phe Phe Gln
 1 5

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp
 1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1007 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala
 1 5 10 15

Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp
 20 25 30
 Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys
 35 40 45
 Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr
 50 55 60
 Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu
 65 70 75 80
 Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val
 85 90 95
 Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys
 100 105 110
 Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu
 115 120 125
 Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn
 130 135 140
 Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr
 145 150 155 160
 Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe
 165 170 175
 Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp
 180 185 190
 Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys
 195 200 205
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn
 210 215 220
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile
 225 230 235 240
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His
 245 250 255
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln
 260 265 270
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu
 275 280 285
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys
 290 295 300
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu
 305 310 315 320
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr
 325 330 335

Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr
 340 345 350
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile
 355 360 365
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys
 370 375 380
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys
 385 390 395 400
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln
 405 410 415
 Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile
 420 425 430
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val
 435 440 445
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr
 450 455 460
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys
 465 470 475 480
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu
 485 490 495
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
 500 505 510
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
 515 520 525
 Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
 530 535 540
 Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn
 545 550 555 560
 Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp
 565 570 575
 Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly
 580 585 590
 Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 595 600 605
 Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu
 610 615 620
 Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys
 625 630 635 640
 Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys
 645 650 655

Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln
 660 665 670
 Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn
 675 680 685
 Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys
 690 695 700
 Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr
 705 710 715 720
 Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln
 725 730 735
 Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu
 740 745 750
 Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu
 755 760 765
 Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu
 770 775 780
 Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile
 785 790 795 800
 Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln
 805 810 815
 Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp
 820 825 830
 Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly
 835 840 845
 Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu
 850 855 860
 Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys
 865 870 875 880
 Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn
 885 890 895
 Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala
 900 905 910
 Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met
 915 920 925
 Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met
 930 935 940
 Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr
 945 950 955 960
 Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe
 965 970 975

Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe
 980 985 990

Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
 995 1000 1005

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg
 1 5 10 15

Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala
 20 25 30

Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg
 35 40 45

Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu
 50 55 60

Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg
 65 70 75 80

Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys Asn Thr
 85 90 95

Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn
 100 105 110

Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp
 115 120 125

Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp
 130 135 140

Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg
 145 150 155 160

Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr
 165 170 175

Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn
 180 185 190

Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn Leu Leu
 195 200 205

Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu
 210 215 220

Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro
 225 230 235 240
 Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His
 245 250 255
 Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu
 260 265 270
 Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu
 275 280 285
 Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu
 290 295 300
 Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu
 305 310 315 320
 Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn
 325 330 335
 Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile
 340 345 350
 Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn
 355 360 365
 Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val Ile Asn
 370 375 380
 Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu
 385 390 395 400
 Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly
 405 410 415
 Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu
 420 425 430
 Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met
 435 440 445
 Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly
 450 455 460
 Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala
 465 470 475 480
 Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser
 485 490 495
 Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys
 500 505 510
 Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu
 515 520 525
 Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser
 530 535 540

Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly
 545 550 555 560
 Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys
 565 570 575
 Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr
 580 585 590
 Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp Met Met
 595 600 605
 Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val
 610 615 620
 Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile
 625 630 635 640
 Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp
 645 650 655
 Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser
 660 665 670
 Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu
 675 680 685
 Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly
 690 695

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn Gln Val
 1 5 10 15
 Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr Lys Tyr
 20 25 30
 Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe Cys Gly
 35 40 45
 Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp Lys Lys
 50 55 60
 Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys Ser Thr
 65 70 75 80
 Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn Asn Ile
 85 90 95

Asn	Val	Pro	Asn	Trp	Asn	Asn	Met	Lys	Ser	Arg	Thr	Arg	Ile	Phe	Tyr	100	105	110
Cys	Thr	His	Phe	Asn	Arg	Asn	Asn	Gln	Phe	Phe	Lys	Lys	His	Glu	Phe	115	120	125
Val	Ser	Asn	Lys	Asn	Asn	Ile	Ser	Ala	Met	Asp	Arg	Ala	Gln	Thr	Ile	130	135	140
Phe	Thr	Asn	Ile	Phe	Arg	Phe	Asn	Arg	Ile	Arg	Lys	Lys	Leu	Lys	Asp	145	150	155
Lys	Val	Ile	Glu	Lys	Ile	Ala	Tyr	Met	Leu	Glu	Lys	Val	Lys	Asp	Phe	165	170	175
Asn	Phe	Asn	Tyr	Tyr	Leu	Thr	Lys	Ser	Cys	Pro	Leu	Pro	Glu	Asn	Trp	180	185	190
Arg	Glu	Arg	Lys	Gln	Lys	Ile	Glu	Asn	Leu	Ile	Asn	Lys	Thr	Arg	Glu	195	200	205
Glu	Lys	Ser	Lys	Tyr	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Thr	Thr	Asp	Asn	210	215	220
Lys	Cys	Val	Thr	Gln	Phe	Ile	Asn	Glu	Phe	Phe	Tyr	Asn	Ile	Leu	Pro	225	230	235
Lys	Asp	Phe	Leu	Thr	Gly	Arg	Asn	Arg	Lys	Asn	Phe	Gln	Lys	Lys	Val	245	250	255
Lys	Lys	Tyr	Val	Glu	Leu	Asn	Lys	His	Glu	Leu	Ile	His	Lys	Asn	Leu	260	265	270
Leu	Leu	Glu	Lys	Ile	Asn	Thr	Arg	Glu	Ile	Ser	Trp	Met	Gln	Val	Glu	275	280	285
Thr	Ser	Ala	Lys	His	Phe	Tyr	Tyr	Phe	Asp	His	Glu	Asn	Ile	Tyr	Val	290	295	300
Leu	Trp	Lys	Leu	Leu	Arg	Trp	Ile	Phe	Glu	Asp	Leu	Val	Val	Ser	Leu	305	310	315
Ile	Arg	Cys	Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys	325	330	335
Thr	Tyr	Tyr	Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser	340	345	350
Ile	Ala	Asp	Leu	Lys	Lys	Glu	Thr	Leu	Ala	Glu	Val	Gln	Glu	Lys	Glu	355	360	365
Val	Glu	Glu	Trp	Lys	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg	370	375	380
Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys	385	390	395
Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	Asn	Thr	405	410	415

Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met
 420 425 430
 Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met
 435 440 445
 Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro
 450 455 460
 Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
 465 470 475 480
 Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser
 485 490 495
 Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn
 500 505 510
 Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr
 515 520 525
 Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro
 530 535 540
 Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys
 545 550 555 560
 Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp
 565 570 575
 Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn
 580 585 590
 Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu
 595 600 605
 Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu
 610 615 620
 Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro
 625 630 635 640
 Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr
 645 650 655
 Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val
 660 665 670
 Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser
 675 680 685
 Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val
 690 695 700
 Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser
 705 710 715 720
 Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile
 725 730 735

Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala
 740 745 750
 Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile
 755 760 765
 Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys
 770 775 780
 Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys
 785 790 795 800
 Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser
 805 810 815
 Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala
 820 825 830
 Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu
 835 840 845
 Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu
 850 855 860
 Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu
 865 870 875 880
 Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile
 885 890 895
 Gln

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1 5 10 15
 Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30
 Ile Glu His Tyr Lys Thr Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80

Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125
 Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
 130 135 140
 Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
 145 150 155 160
 Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
 165 170 175
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
 180 185 190
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
 195 200 205
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
 385 390 395 400

Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
 530 535 540
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
 545 550 555 560
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
 565 570 575
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
 580 585 590
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
 595 600 605
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
 610 615 620
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
 625 630 635 640
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
 645 650 655
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
 660 665 670
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
 675 680 685
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
 690 695 700
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
 705 710 715 720

Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys
 835 840

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn
 1 5 10 15
 Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys
 20 25 30
 Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln
 35 40 45
 Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu
 50 55 60
 Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr
 65 70 75 80
 Leu Leu Met

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser Leu Glu Ser Leu Glu
1           5           10           15

Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser Cys Lys Asn Leu Gln
          20           25           30

Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro Asn Asn Ile Gln Lys
          35           40           45

Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe Lys Gln Phe Glu Gln
          50           55           60

Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys Ile Leu Asp Gln His
65           70           75           80

Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys Asn Lys Lys Ile Lys
          85           90           95

Ala Phe Ile Leu
          100

```

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

Met Glu Met Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn
1           5           10           15

Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys
          20           25           30

Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu
          35           40           45

Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp
          50           55           60

```

Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu
65 70 75 80

Ile Glu Thr Leu Leu
85

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu Asp Glu Ile
1 5 10 15

Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser Met Ser Thr
20 25 30

Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu
35 40 45

Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys
50 55 60

Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys
65 70 75 80

Tyr Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro Ser Met Gln
85 90 95

Lys Leu Leu

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif A"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 4

(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 6

(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 13

(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5								10

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
      (A) NAME/KEY: Peptide
      (B) LOCATION: 1..13
      (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
                               from motif B"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 1
      (D) OTHER INFORMATION: /product= "OTHER"
                             /note= "Xaa = hydrophobic amino acid,
                             Ala, Leu, Ile, Val, Pro, Phe, Trp
                             or Met"
```

Xaa Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Pro
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..10
(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif C"

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

```
(A) NAME/KEY: Modified-site
(B) LOCATION: 8..10
(D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = hydrophobic amino acid,
                        Ala, Leu, Ile, Val, Pro, Phe, Trp
                        or Met"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Xaa Xaa Xaa Tyr Xaa Asp Asp Xaa Xaa Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..8
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif D"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe, Trp
 or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe, Trp
 or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..8
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif E"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Xaa Xaa Xaa Leu Gly Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from Dong (LINE)"

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe
1 5 10 15
Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys
20 25 30
Ile Asn

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

```
(A) NAME/KEY: Peptide
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /note= "motif B peptide from
                        Dong (LINE)"
```

Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser Leu Ser
1 5 10 15
Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln Leu His
20 25 30
Asn Asp Arg
35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

```
(A) NAME/KEY: Peptide
(B) LOCATION: 1..43
(D) OTHER INFORMATION: /note= "motif C and D peptide from
                        Dong (LINE)"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys
 1 5 10 15
 Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile
 20 25 30
 Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
Dong (LINE)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Lys Cys Leu Tyr Lys Tyr Leu Gly Phe Gln Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe
 1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
 20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B peptide from
 Saccharomyces cerevisiae cytochrome
 oxidase group II intron 1-encoded
 mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro Thr Ser
 1 5 10 15

Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg Leu Ala
 20 25 30

Gly Leu Ala
 35

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif D peptide from
 Saccharomyces cerevisiae cytochrome
 oxidase group II intron 1-encoded
 mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu
 1 5 10 15
 Thr Ile Asn Glu Glu Lys Thr Leu Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from HIV RT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr
 1 5 10 15
 Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr
 20 25 30
 Ile Pro

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B peptide from HIV RT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser
 1 5 10 15
 Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg
 20 25 30

Lys Gln Asn
35

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..17
 (D) OTHER INFORMATION: /note= "motif C peptide from HIV RT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile
 1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..37
 (D) OTHER INFORMATION: /note= "motif D and E peptide from
 HIV RT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
 1 5 10 15

Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
 20 25 30

Met Gly Tyr Glu Leu
 35

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: /note= "motif C and D peptide from
Saccharomyces cerevisiae
ESTp (L8543.12)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1           5           10           15
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
          20           25           30
Asn Ala Lys Ala Asn Arg
          35

```

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
Saccharomyces cerevisiae
ESTp (L8543.12)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe Arg
1           5           10

```

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn
 1 5 10 15
 Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val
 20 25 30
 Glu Ile Glu Thr Leu Leu Met
 35

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Ile Cys His Gln Xaa Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg
 1 5 10 15
 Asp Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro
 20 25 30
 Leu Glu Ile Met Ile Lys
 35

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg
 1 5 10 15

Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro
 20 25 30

Leu Glu Thr Met Ile Lys
 35

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Ile Leu Arg Gln Val Glu Tyr Tyr Phe Gly Asp Ala Asn Leu Asn Arg
 1 5 10 15

Asp Lys Phe Leu Arg Glu Gln Ile Gly Lys Asn Glu Asp Gly Trp Val
 20 25 30

Pro Leu Ser Val Leu Val Thr
 35

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Cys Leu Lys Gln Val Glu Phe Tyr Phe Ser Glu Phe Asn Phe Pro Tyr
 1 5 10 15

Asp Arg Phe Leu Arg Thr Thr Ala Glu Lys Asn Asp Gly Trp Val Pro
 20 25 30

Ile Ser Thr Ile Ala Thr
 35

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2421 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 92..2251

(D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)
/codon= (seq: "tag", aa: Gln)
/codon= (seq: "tga", aa: TRM)
/product= "Tetrahymena thermophila
80 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

AACTCATTTA ATTACTAATT TAATCAACAA GATTGATAAA AAGCAGTAAA TAAAACCCAA	60
TAGATTTAAT TTAGAAAGTA TCAATTGAAA A ATG GAA ATT GAA AAC AAC TAA	112
Met Glu Ile Glu Asn Asn Gln	
1 5	
GCA CAA TAG CCA AAA GCC GAA AAA TTG TGG TGG GAA CTT GAA TTA GAG	160
Ala Gln Gln Pro Lys Ala Glu Lys Leu Trp Trp Glu Leu Glu Leu Glu	
10 15 20	
ATG CAA GAA AAC CAA AAT GAT ATA TAA GTT AGG GTT AAG ATT GAC GAT	208
Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg Val Lys Ile Asp Asp	
25 30 35	
CCT AAG CAA TAT CTC GTG AAC GTC ACT GCA GCA TGT TTG TTG TAG GAA	256
Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala Cys Leu Leu Gln Glu	
40 45 50 55	
GGT AGT TAC TAC TAA GAT AAA GAT GAA AGA AGA TAT ATC ATC ACT AAA	304
Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg Tyr Ile Ile Thr Lys	
60 65 70	
GCA CTT CTT GAG GTG GCT GAG TCT GAT CCT GAG TTC ATC TGC TAG TTG	352
Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu Phe Ile Cys Gln Leu	
75 80 85	
GCA GTC TAC ATC CGT AAT GAA CTT TAC ATC AGA ACT ACC ACT AAC TAC	400
Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg Thr Thr Thr Asn Tyr	
90 95 100	
ATT GTA GCA TTT TGT GTT GTC CAC AAG AAT ACT CAA CCA TTC ATC GAA	448
Ile Val Ala Phe Cys Val Val His Lys Asn Thr Gln Pro Phe Ile Glu	
105 110 115	
AAG TAC TTC AAC AAA GCA GTA CTT TTG CCT AAT GAC TTA CTG GAA GTC	496
Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn Asp Leu Leu Glu Val	
120 125 130 135	
TGT GAA TTT GCA TAG GTT CTC TAT ATT TTT GAT GCA ACT GAA TTC AAA	544
Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp Ala Thr Glu Phe Lys	
140 145 150	
AAT TTG TAT CTT GAT AGG ATA CTT TCA TAA GAT ATT CGT AAG GAA CTC	592
Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp Ile Arg Lys Glu Leu	
155 160 165	

ACT	TTC	CGT	AAG	TGT	TTA	CAA	AGA	TGC	GTC	AGA	AGC	AAG	TTT	TCT	GAA	640
Thr	Phe	Arg	Lys	Cys	Leu	Gln	Arg	Cys	Val	Arg	Ser	Lys	Phe	Ser	Glu	
		170					175					180				
TTC	AAC	GAA	TAC	TAA	CTT	GGT	AAG	TAT	TGC	ACT	GAA	TCC	TAA	CGT	AAG	688
Phe	Asn	Glu	Tyr	Gln	Leu	Gly	Lys	Tyr	Cys	Thr	Glu	Ser	Gln	Arg	Lys	
	185					190					195					
AAA	ACA	ATG	TTC	CGT	TAC	CTC	TCA	GTT	ACC	AAC	AAG	TAA	AAG	TGG	GAT	736
Lys	Thr	Met	Phe	Arg	Tyr	Leu	Ser	Val	Thr	Asn	Lys	Gln	Lys	Trp	Asp	
200					205					210					215	
TAA	ACT	AAG	AAG	AAG	AGA	AAA	GAG	AAT	CTC	TTA	ACC	AAA	CTT	TAG	GCA	784
Gln	Thr	Lys	Lys	Lys	Arg	Lys	Glu	Asn	Leu	Leu	Thr	Lys	Leu	Gln	Ala	
				220					225					230		
ATA	AAG	GAA	TCT	GAA	GAT	AAG	TCC	AAG	AGA	GAA	ACT	GGA	GAC	ATA	ATG	832
Ile	Lys	Glu	Ser	Glu	Asp	Lys	Ser	Lys	Arg	Glu	Thr	Gly	Asp	Ile	Met	
			235					240					245			
AAC	GTT	GAA	GAT	GCA	ATC	AAG	GCT	TTA	AAA	CCA	GCA	GTT	ATG	AAG	AAA	880
Asn	Val	Glu	Asp	Ala	Ile	Lys	Ala	Leu	Lys	Pro	Ala	Val	Met	Lys	Lys	
		250					255					260				
ATA	GCC	AAG	AGA	TAG	AAT	GCC	ATG	AAG	AAA	CAC	ATG	AAG	GCA	CCT	AAA	928
Ile	Ala	Lys	Arg	Gln	Asn	Ala	Met	Lys	Lys	His	Met	Lys	Ala	Pro	Lys	
	265					270					275					
ATT	CCT	AAC	TCT	ACC	TTG	GAA	TCA	AAG	TAC	TTG	ACC	TTC	AAG	GAT	CTC	976
Ile	Pro	Asn	Ser	Thr	Leu	Glu	Ser	Lys	Tyr	Leu	Thr	Phe	Lys	Asp	Leu	
280					285					290					295	
ATT	AAG	TTC	TGC	CAT	ATT	TCT	GAG	CCT	AAA	GAA	AGA	GTC	TAT	AAG	ATC	1024
Ile	Lys	Phe	Cys	His	Ile	Ser	Glu	Pro	Lys	Glu	Arg	Val	Tyr	Lys	Ile	
				300					305					310		
CTT	GGT	AAA	AAA	TAC	CCT	AAG	ACC	GAA	GAG	GAA	TAC	AAA	GCA	GCC	TTT	1072
Leu	Gly	Lys	Lys	Tyr	Pro	Lys	Thr	Glu	Glu	Glu	Tyr	Lys	Ala	Ala	Phe	
			315					320					325			
GGT	GAT	TCT	GCA	TCT	GCA	CCC	TTC	AAT	CCT	GAA	TTG	GCT	GGA	AAG	CGT	1120
Gly	Asp	Ser	Ala	Ser	Ala	Pro	Phe	Asn	Pro	Glu	Leu	Ala	Gly	Lys	Arg	
		330					335					340				
ATG	AAG	ATT	GAA	ATC	TCT	AAA	ACA	TGG	GAA	AAT	GAA	CTC	AGT	GCA	AAA	1168
Met	Lys	Ile	Glu	Ile	Ser	Lys	Thr	Trp	Glu	Asn	Glu	Leu	Ser	Ala	Lys	
	345					350					355					
GGC	AAC	ACT	GCT	GAG	GTT	TGG	GAT	AAT	TTA	ATT	TCA	AGC	AAT	TAA	CTC	1216
Gly	Asn	Thr	Ala	Glu	Val	Trp	Asp	Asn	Leu	Ile	Ser	Ser	Asn	Gln	Leu	
360					365					370					375	
CCA	TAT	ATG	GCC	ATG	TTA	CGT	AAC	TTG	TCT	AAC	ATC	TTA	AAA	GCC	GGT	1264
Pro	Tyr	Met	Ala	Met	Leu	Arg	Asn	Leu	Ser	Asn	Ile	Leu	Lys	Ala	Gly	
				380					385					390		
GTT	TCA	GAT	ACT	ACA	CAC	TCT	ATT	GTG	ATC	AAC	AAG	ATT	TGT	GAG	CCC	1312
Val	Ser	Asp	Thr	Thr	His	Ser	Ile	Val	Ile	Asn	Lys	Ile	Cys	Glu	Pro	
			395					400						405		

AAG GCC GTT GAG AAC TCC AAG ATG TTC CCT CTT CAA TTC TTT AGT GCC Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu Gln Phe Phe Ser Ala 410 415 420	1360
ATT GAA GCT GTT AAT GAA GCA GTT ACT AAG GGA TTC AAG GCC AAG AAG Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly Phe Lys Ala Lys Lys 425 430 435	1408
AGA GAA AAT ATG AAT CTT AAA GGT CAA ATC GAA GCA GTA AAG GAA GTT Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu Ala Val Lys Glu Val 440 445 450 455	1456
GTT GAA AAA ACC GAT GAA GAG AAG AAA GAT ATG GAG TTG GAG TAA ACC Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met Glu Leu Glu Gln Thr 460 465 470	1504
GAA GAA GGA GAA TTT GTT AAA GTC AAC GAA GGA ATT GGC AAG CAA TAC Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly Ile Gly Lys Gln Tyr 475 480 485	1552
ATT AAC TCC ATT GAA CTT GCA ATC AAG ATA GCA GTT AAC AAG AAT TTA Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu 490 495 500	1600
GAT GAA ATC AAA GGA CAC ACT GCA ATC TTC TCT GAT GTT TCT GGT TCT Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser 505 510 515	1648
ATG AGT ACC TCA ATG TCA GGT GGA GCC AAG AAG TAT GGT TCC GTT CGT Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg 520 525 530 535	1696
ACT TGT CTC GAG TGT GCA TTA GTC CTT GGT TTG ATG GTA AAA TAA CGT Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg 540 545 550	1744
TGT GAA AAG TCC TCA TTC TAC ATC TTC AGT TCA CCT AGT TCT CAA TGC Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys 555 560 565	1792
AAT AAG TGT TAC TTA GAA GTT GAT CTC CCT GGA GAC GAA CTC CGT CCT Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro 570 575 580	1840
TCT ATG TAA AAA CTT TTG CAA GAG AAA GGA AAA CTT GGT GGT GGT ACT Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys Leu Gly Gly Gly Thr 585 590 595	1888
GAT TTC CCC TAT GAG TGC ATT GAT GAA TGG ACA AAG AAT AAA ACT CAC Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr Lys Asn Lys Thr His 600 605 610 615	1936
GTA GAC AAT ATC GTT ATT TTG TCT GAT ATG ATG ATT GCA GAA GGA TAT Val Asp Asn Ile Val Ile Leu Ser Asp Met Met Ile Ala Glu Gly Tyr 620 625 630	1984
TCA GAT ATC AAT GTT AGA GGC AGT TCC ATT GTT AAC AGC ATC AAA AAG Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val Asn Ser Ile Lys Lys 635 640 645	2032

TAC AAG GAT GAA GTA AAT CCT AAC ATT AAA ATC TTT GCA GTT GAC TTA	2080
Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile Phe Ala Val Asp Leu	
650 655 660	
GAA GGT TAC GGA AAG TGC CTT AAT CTA GGT GAT GAG TTC AAT GAA AAC	2128
Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp Glu Phe Asn Glu Asn	
665 670 675	
AAC TAC ATC AAG ATA TTC GGT ATG AGC GAT TCA ATC TTA AAG TTC ATT	2176
Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser Ile Leu Lys Phe Ile	
680 685 690 695	
TCA GCC AAG CAA GGA GGA GCA AAT ATG GTC GAA GTT ATC AAA AAC TTT	2224
Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu Val Ile Lys Asn Phe	
700 705 710	
GCC CTT CAA AAA ATA GGA CAA AAG TGAGTTTCTT GAGATTCTTC TATAACAAAA	2278
Ala Leu Gln Lys Ile Gly Gln Lys	
715	
ATCTCACCCC ACTTTTTTGT TTTATTGCAT AGCCATTATG AAATTTAAAT TATTATCTAT	2338
TTATTTAAGT TACTTACATA GTTTATGTAT CGCAGTCTAT TAGCCTATTC AAATGATTCT	2398
GCAAAGAACA AAAAAGATTA AAA	2421

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Glu Ile Glu Asn Asn Gln Ala Gln Gln Pro Lys Ala Glu Lys Leu	
1 5 10 15	
Trp Trp Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln	
20 25 30	
Val Arg Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr	
35 40 45	
Ala Ala Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu	
50 55 60	
Arg Arg Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp	
65 70 75 80	
Pro Glu Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr	
85 90 95	
Ile Arg Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys	
100 105 110	
Asn Thr Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu	
115 120 125	

Pro Asn Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile
 130 135 140

Phe Asp Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser
 145 150 155 160

Gln Asp Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys
 165 170 175

Val Arg Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr
 180 185 190

Cys Thr Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val
 195 200 205

Thr Asn Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn
 210 215 220

Leu Leu Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys
 225 230 235 240

Arg Glu Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu
 245 250 255

Lys Pro Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys
 260 265 270

Lys His Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys
 275 280 285

Tyr Leu Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro
 290 295 300

Lys Glu Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu
 305 310 315 320

Glu Glu Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn
 325 330 335

Pro Glu Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp
 340 345 350

Glu Asn Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn
 355 360 365

Leu Ile Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu
 370 375 380

Ser Asn Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val
 385 390 395 400

Ile Asn Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe
 405 410 415

Pro Leu Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr
 420 425 430

Lys Gly Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln
 435 440 445

Ile Glu Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys
 450 455 460
 Asp Met Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn
 465 470 475 480
 Glu Gly Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys
 485 490 495
 Ile Ala Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile
 500 505 510
 Phe Ser Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala
 515 520 525
 Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu
 530 535 540
 Gly Leu Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe
 545 550 555 560
 Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu
 565 570 575
 Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys
 580 585 590
 Gly Lys Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu
 595 600 605
 Trp Thr Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp
 610 615 620
 Met Met Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser
 625 630 635 640
 Ile Val Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile
 645 650 655
 Lys Ile Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu
 660 665 670
 Gly Asp Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser
 675 680 685
 Asp Ser Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met
 690 695 700
 Val Glu Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly Gln Lys
 705 710 715

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 47..2665

(D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)
 /codon= (seq: "tag", aa: Gln)
 /codon= (seq: "tga", aa: TRM)
 /product= "Tetrahymena thermophila
 95 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TCAATACTAT TAATTAATAA ATAAAAAAAA GCAAACCTACA AAGAAA ATG TCA AGG	55
Met Ser Arg	
1	
CGT AAC TAA AAA AAG CCA TAG GCT CCT ATA GGC AAT GAA ACA AAT CTT	103
Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu Thr Asn Leu	
5 10 15	
GAT TTT GTA TTA CAA AAT CTA GAA GTT TAC AAA AGC CAG ATT GAG CAT	151
Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln Ile Glu His	
20 25 30 35	
TAT AAG ACC TAG TAG TAA TAG ATC AAA GAG GAG GAT CTC AAG CTT TTA	199
Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu Lys Leu Leu	
40 45 50	
AAG TTC AAA AAT TAA GAT TAG GAT GGA AAC TCT GGC AAC GAT GAT GAT	247
Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn Asp Asp Asp	
55 60 65	
GAT GAA GAA AAC AAC TCA AAT AAA TAA TAA GAA TTA TTA AGG AGA GTC	295
Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu Arg Arg Val	
70 75 80	
AAT TAG ATT AAG TAG CAA GTT TAA TTG ATA AAA AAA GTT GGT TCT AAG	343
Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val Gly Ser Lys	
85 90 95	
GTA GAG AAA GAT TTG AAT TTG AAC GAA GAT GAA AAC AAA AAG AAT GGA	391
Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys Lys Asn Gly	
100 105 110 115	
CTT TCT GAA TAG CAA GTG AAA GAA GAG TAA TTA AGA ACG ATT ACT GAA	439
Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr Ile Thr Glu	
120 125 130	
GAA TAG GTT AAG TAT TAA AAT TTA GTA TTT AAC ATG GAC TAC CAG TTA	487
Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp Tyr Gln Leu	
135 140 145	
GAT TTA AAT GAG AGT GGT GGC CAT AGA AGA CAC AGA AGA GAA ACA GAT	535
Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg Glu Thr Asp	
150 155 160	
TAT GAT ACT GAA AAA TGG TTT GAA ATA TCT CAT GAC CAA AAA AAT TAT	583
Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln Lys Asn Tyr	
165 170 175	

GTA TCA ATT TAC GCC AAC TAA AAG ACA TCA TAT TGT TGG TGG CTT AAA	631
Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp Trp Leu Lys	
180 185 190 195	
GAT TAT TTT AAT AAA AAC AAT TAT GAT CAT CTT AAT GTA AGC ATT AAC	679
Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val Ser Ile Asn	
200 205 210	
AGA CTA GAA ACT GAA GCC GAA TTC TAT GCC TTT GAT GAT TTT TCA CAA	727
Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp Phe Ser Gln	
215 220 225	
ACA ATC AAA CTT ACT AAT AAT TCT TAC TAG ACT GTT AAC ATA GAC GTT	775
Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn Ile Asp Val	
230 235 240	
AAT TTT GAT AAT AAT CTC TGT ATA CTC GCA TTG CTT AGA TTT TTA TTA	823
Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg Phe Leu Leu	
245 250 255	
TCA CTA GAA AGA TTC AAT ATT TTG AAT ATA AGA TCT TCT TAT ACA AGA	871
Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser Tyr Thr Arg	
260 265 270 275	
AAT TAA TAT AAT TTT GAG AAA ATT GGT GAG CTA CTT GAA ACT ATC TTC	919
Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu Thr Ile Phe	
280 285 290	
GCA GTT GTC TTT TCT CAT CGC CAC TTA CAA GGC ATT CAT TTA CAA GTT	967
Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His Leu Gln Val	
295 300 305	
CCT TGC GAA GCG TTC TAA TAT TTA GTT AAC TCC TCA TCA TAA ATT AGC	1015
Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser Gln Ile Ser	
310 315 320	
GTT AAA GAT AGC TAA TTA TAG GTA TAC TCT TTC TCT ACA GAC TTA AAA	1063
Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr Asp Leu Lys	
325 330 335	
TTA GTT GAC ACT AAC AAA GTC CAA GAT TAT TTT AAG TTC TTA TAA GAA	1111
Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe Leu Gln Glu	
340 345 350 355	
TTC CCT CGT TTG ACT CAT GTA AGC TAG TAG GCT ATC CCA GTT AGT GCT	1159
Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro Val Ser Ala	
360 365 370	
ACT AAC GCT GTA GAG AAC CTC AAT GTT TTA CTT AAA AAG GTC AAG CAT	1207
Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys Val Lys His	
375 380 385	
GCT AAT CTT AAT TTA GTT TCT ATC CCT ACC TAA TTC AAT TTT GAT TTC	1255
Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn Phe Asp Phe	
390 395 400	
TAC TTT GTT AAT TTA TAA CAT TTG AAA TTA GAG TTT GGA TTA GAA CCA	1303
Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly Leu Glu Pro	
405 410 415	

AAT ATT TTG ACA AAA CAA AAG CTT GAA AAT CTA CTT TTG AGT ATA AAA Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Ser Ile Lys 420 425 430 435	1351
TAA TCA AAA AAT CTT AAA TTT TTA AGA TTA AAC TTT TAC ACC TAC GTT Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr Thr Tyr Val 440 445 450	1399
GCT TAA GAA ACC TCC AGA AAA CAG ATA TTA AAA CAA GCT ACA ACA ATC Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala Thr Thr Ile 455 460 465	1447
AAA AAT CTC AAA AAC AAT AAA AAT CAA GAA GAA ACT CCT GAA ACT AAA Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro Glu Thr Lys 470 475 480	1495
GAT GAA ACT CCA AGC GAA AGC ACA AGT GGT ATG AAA TTT TTT GAT CAT Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe Phe Asp His 485 490 495	1543
CTT TCT GAA TTA ACC GAG CTT GAA GAT TTC AGC GTT AAC TTG TAA GCT Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn Leu Gln Ala 500 505 510 515	1591
ACC CAA GAA ATT TAT GAT AGC TTG CAC AAA CTT TTG ATT AGA TCA ACA Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile Arg Ser Thr 520 525 530	1639
AAT TTA AAG AAG TTC AAA TTA AGT TAC AAA TAT GAA ATG GAA AAG AGT Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met Glu Lys Ser 535 540 545	1687
AAA ATG GAT ACA TTC ATA GAT CTT AAG AAT ATT TAT GAA ACC TTA AAC Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu Thr Leu Asn 550 555 560	1735
AAT CTT AAA AGA TGC TCT GTT AAT ATA TCA AAT CCT CAT GGA AAC ATT Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His Gly Asn Ile 565 570 575	1783
TCT TAT GAA CTG ACA AAT AAA GAT TCT ACT TTT TAT AAA TTT AAG CTG Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys Phe Lys Leu 580 585 590 595	1831
ACC TTA AAC TAA GAA TTA TAA CAC GCT AAG TAT ACT TTT AAG TAG AAC Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe Lys Gln Asn 600 605 610	1879
GAA TTT TAA TTT AAT AAC GTT AAA AGT GCA AAA ATT GAA TCT TCC TCA Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser 615 620 625	1927
TTA GAA AGC TTA GAA GAT ATT GAT AGT CTT TGC AAA TCT ATT GCT TCT Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser 630 635 640	1975
TGT AAA AAT TTA CAA AAT GTT AAT ATT ATC GCC AGT TTG CTC TAT CCC Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro 645 650 655	2023

AAC AAT ATT TAG AAA AAT CCT TTC AAT AAG CCC AAT CTT CTA TTT TTC Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe 660 665 670 675	2071
AAG CAA TTT GAA TAA TTG AAA AAT TTG GAA AAT GTA TCT ATC AAC TGT Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys 680 685 690	2119
ATT CTT GAT CAG CAT ATA CTT AAT TCT ATT TCA GAA TTC TTA GAA AAG Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys 695 700 705	2167
AAT AAA AAA ATA AAA GCA TTC ATT TTG AAA AGA TAT TAT TTA TTA CAA Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr Leu Leu Gln 710 715 720	2215
TAT TAT CTT GAT TAT ACT AAA TTA TTT AAA ACA CTT CAA TAG TTA CCT Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln Gln Leu Pro 725 730 735	2263
GAA TTA AAT TAA GTT TAC ATT AAT TAG CAA TTA GAA GAA TTG ACT GTG Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu Leu Thr Val 740 745 750 755	2311
AGT GAA GTA CAT AAG TAA GTA TGG GAA AAC CAC AAG CAA AAA GCT TTC Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln Lys Ala Phe 760 765 770	2359
TAT GAA CCA TTA TGT GAG TTT ATC AAA GAA TCA TCC TAA ACC CTT TAG Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln Thr Leu Gln 775 780 785	2407
CTA ATA GAT TTT GAC CAA AAC ACT GTA AGT GAT GAC TCT ATT AAA AAG Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser Ile Lys Lys 790 795 800	2455
ATT TTA GAA TCT ATA TCT GAG TCT AAG TAT CAT CAT TAT TTG AGA TTG Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr Leu Arg Leu 805 810 815	2503
AAC CCT AGT TAA TCT AGC AGT TTA ATT AAA TCT GAA AAC GAA GAA ATT Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn Glu Glu Ile 820 825 830 835	2551
TAA GAA CTT CTC AAA GCT TGC GAC GAA AAA GGT GTT TTA GTA AAA GCA Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu Val Lys Ala 840 845 850	2599
TAC TAT AAA TTC CCT CTA TGT TTA CCA ACT GGT ACT TAT TAC GAT TAC Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr Tyr Asp Tyr 855 860 865	2647
AAT TCA GAT AGA TGG TGATTAATTA AATATTAGTT TAAATAAATA TTAAATATTG Asn Ser Asp Arg Trp 870	2702
AATATTTCTT TGCTTATTAT TTGAATAATA CATACAATAG TCATTTTGTAG TGTTTTGAAT	2762
ATATTTTAGT TATTTAATTC ATTATTTTAA GTAAATAATT ATTTTTCAT CATTTTTAA	2822
AAAATCG	2829

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

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Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1             5             10             15
Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
      20             25             30
Ile Glu His Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu
      35             40             45
Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
      50             55             60
Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
      65             70             75             80
Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
      85             90             95
Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
      100            105            110
Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
      115            120            125
Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
      130            135            140
Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
      145            150            155            160
Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
      165            170            175
Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
      180            185            190
Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
      195            200            205
Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
      210            215            220
Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
      225            230            235            240
Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
      245            250            255
Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
      260            265            270

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Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
 385 390 395 400
 Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
 530 535 540
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
 545 550 555 560
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
 565 570 575
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
 580 585 590

Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
 595 600 605
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
 610 615 620
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
 625 630 635 640
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
 645 650 655
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
 660 665 670
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
 675 680 685
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
 690 695 700
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
 705 710 715 720
 Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu
 835 840 845
 Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr
 850 855 860
 Tyr Asp Tyr Asn Ser Asp Arg Trp
 865 870

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..884
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae
ESTp (L8543.12)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

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Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
1           5           10           15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn
20          25          30

Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
35          40          45

Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
50          55          60

Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
65          70          75          80

Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
85          90          95

Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
100         105         110

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
115         120         125

Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
130         135         140

Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
145         150         155         160

Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
165         170         175

Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
180         185         190

Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
195         200         205

Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
210         215         220

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Asn	Leu	Val	Lys	Ile	Pro	Gln	Arg	Leu	Lys	Val	Arg	Ile	Asn	Leu	Thr	225	230	235	240
Leu	Gln	Lys	Leu	Leu	Lys	Arg	His	Lys	Arg	Leu	Asn	Tyr	Val	Ser	Ile	245	250	255	
Leu	Asn	Ser	Ile	Cys	Pro	Pro	Leu	Glu	Gly	Thr	Val	Leu	Asp	Leu	Ser	260	265	270	
His	Leu	Ser	Arg	Gln	Ser	Pro	Lys	Glu	Arg	Val	Leu	Lys	Phe	Ile	Ile	275	280	285	
Val	Ile	Leu	Gln	Lys	Leu	Leu	Pro	Gln	Glu	Met	Phe	Gly	Ser	Lys	Lys	290	295	300	
Asn	Lys	Gly	Lys	Ile	Ile	Lys	Asn	Leu	Asn	Leu	Leu	Leu	Ser	Leu	Pro	305	310	315	320
Leu	Asn	Gly	Tyr	Leu	Pro	Phe	Asp	Ser	Leu	Leu	Lys	Lys	Leu	Arg	Leu	325	330	335	
Lys	Asp	Phe	Arg	Trp	Leu	Phe	Ile	Ser	Asp	Ile	Trp	Phe	Thr	Lys	His	340	345	350	
Asn	Phe	Glu	Asn	Leu	Asn	Gln	Leu	Ala	Ile	Cys	Phe	Ile	Ser	Trp	Leu	355	360	365	
Phe	Arg	Gln	Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr	Cys	Thr	370	375	380	
Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe	Arg	His	Asp	Thr	Trp	385	390	395	400
Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile	Val	Glu	Tyr	Phe	Lys	Thr	Tyr	Leu	405	410	415	
Val	Glu	Asn	Asn	Val	Cys	Arg	Asn	His	Asn	Ser	Tyr	Thr	Leu	Ser	Asn	420	425	430	
Phe	Asn	His	Ser	Lys	Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn	Glu	435	440	445	
Phe	Arg	Ile	Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala	Asp	Glu	Glu	Glu	Phe	450	455	460	
Thr	Ile	Tyr	Lys	Glu	Asn	His	Lys	Asn	Ala	Ile	Gln	Pro	Thr	Gln	Lys	465	470	475	480
Ile	Leu	Glu	Tyr	Leu	Arg	Asn	Lys	Arg	Pro	Thr	Ser	Phe	Thr	Lys	Ile	485	490	495	
Tyr	Ser	Pro	Thr	Gln	Ile	Ala	Asp	Arg	Ile	Lys	Glu	Phe	Lys	Gln	Arg	500	505	510	
Leu	Leu	Lys	Lys	Phe	Asn	Asn	Val	Leu	Pro	Glu	Leu	Tyr	Phe	Met	Lys	515	520	525	
Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	Ile	Pro	Arg	Met	Glu	Cys	Met	530	535	540	

Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
 545 550 555 560
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
 565 570 575
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
 580 585 590
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
 595 600 605
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
 610 615 620
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
 625 630 635 640
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
 645 650 655
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
 660 665 670
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
 675 680 685
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
 690 695 700
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
 705 710 715 720
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
 725 730 735
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
 740 745 750
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
 755 760 765
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
 770 775 780
 His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
 785 790 795 800
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
 805 810 815
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
 820 825 830
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
 835 840 845
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
 850 855 860

Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
 865 870 875 880

His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu
 1 5 10 15

Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys
 20 25 30

Pro Glu Thr Asn Leu Leu Met Arg Leu Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu
 1 5 10 15

Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn
 20 25 30

Pro Asn Val Asn Leu Leu Met Arg Leu Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2631

(D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae
EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

ATTTATACTC ATGAAAATCT TATTCGAGTT CATTCAAGAC AAGCTTGACA TTGATCTACA	60
GACCAACAGT ACTTACAAAG AAAATTTAAA ATGTGGTCAC TTCAATGGCC TCGATGAAAT	120
TCTAACTACG TGTTTCGCAC TACCAAATTC AAGAAAAATA GCATTACCAT GCCTTCCTGG	180
TGACTTAAGC CACAAAGCAG TCATTGATCA CTGCATCATT TACCTGTTGA CGGGCGAATT	240
ATACAACAAC GTACTAACAT TTGGCTATAA AATAGCTAGA AATGAAGATG TCAACAATAG	300
TCTTTTTTGC CATTCTGCAA ATGTTAACGT TACGTTACTG AAAGGCGCTG CTTGGAAAAT	360
GTTCCACAGT TTGGTCGGTA CATACGCATT CGTTGATTTA TTGATCAATT ATACAGTAAT	420
TCAATTTAAT GGGCAGTTTT TCACTCAAAT CGTGGGTAAC AGATGTAACG AACCTCATCT	480
GCCGCCCAAA TGGGTCCAAC GATCATCCTC ATCATCCGCA ACTGCTGCGC AAATCAAACA	540
ACTTACAGAA CCAGTGACAA ATAAACAATT CTTACACAAG CTCATATAA ATTCCTCTTC	600
TTTTTTTCTT TATAGCAAGA TCCTTCCTTC ATCATCATCT ATCAAAAAGC TAACTGACTT	660
GAGAGAAGCT ATTTTTCCCA CAAATTTGGT TAAATTCCT CAGAGACTAA AGGTACGAAT	720
TAATTTGACG CTGCAAAAGC TATTAAAGAG ACATAAGCGT TTGAATTACG TTTCTATTTT	780
GAATAGTATT TGCCCACCAT TGGAAGGGAC CGTATTGGAC TTGTCCGATT TGAGTAGGCA	840
ATCACCAAAG GAACGAGTCT TGAAATTTAT CATTGTTATT TTACAGAAGT TATTACCCCA	900
AGAAATGTTT GGCTCAAAGA AAAATAAAGG AAAAATTATC AAGAATCTAA ATCTTTTATT	960
AAGTTTACCC TTAAATGGCT ATTTACCATT TGATAGTTTG TTGAAAAGT TAAGATTAAA	1020
GGATTTTCGG TGGTTGTTCA TTTCTGATAT TTGGTTCACC AAGCACAATT TTGAAAACCT	1080
GAATCAATTG GCGATTTGTT TCATTTCTCTG GCTATTTAGA CAACTAATTC CCAAATTAT	1140
ACAGACTTTT TTTTACTGCA CCGAAATATC TTCTACAGTG ACAATTGTTT ACTTTAGACA	1200
TGATACTTGG AATAAACTTA TCACCCCTTT TATCGTAGAA TATTTTAAGA CGTACTTAGT	1260
CGAAAACAAC GTATGTAGAA ACCATAATAG TTACACGTTG TCCAATTTCA ATCATAGCAA	1320
AATGAGGATT ATACCAAAAA AAAGTAATAA TGAGTTCAGG ATTATTGCCA TCCCATGCAG	1380
AGGGGCAGAC GAAGAAGAAT TCACAATTTA TAAGGAGAAT CACAAAAATG CTATCCAGCC	1440
CACTCAAAAA ATTTTAGAAT ACCTAAGAAA CAAAAGGCCG ACTAGTTTTA CTAATATATA	1500
TTCTCCAACG CAAATAGCTG ACCGTATCAA AGAATTTAAG CAGAGACTTT TAAAGAAATT	1560

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TAATAATGTC TTACCAGAGC TTTATTTTCAT GAAATTTGAT GTCAAATCTT GCTATGATTC      1620
CATACCAAGG ATGGAATGTA TGAGGATACT CAAGGATGCG CTAAAAAATG AAAATGGGTT      1680
TTTCGTTAGA TCTCAATATT TCTTCAATAC CAATACAGGT GTATTGAAGT TATTTAATGT      1740
TGTTAACGCT AGCAGAGTAC CAAAACCTTA TGAGCTATAC ATAGATAATG TGAGGACGGT      1800
TCATTTATCA AATCAGGATG TTATAAACGT TGTAGAGATG GAAATATTTA AAACAGCTTT      1860
GTGGGTTGAA GATAAGTGCT ACATTAGAGA AGATGGTCTT TTTCAGGGCT CTAGTTTATC      1920
TGCTCCGATC GTTGATTTGG TGTATGACGA TCTTCTGGAG TTTTATAGCG AGTTTAAAGC      1980
CAGTCCTAGC CAGGACACAT TAATTTTAAA ACTGGCTGAC GATTTCTTA TAATATCAAC      2040
AGACCAACAG CAAGTGATCA ATATCAAAAA GCTTGCCATG GCGGATTTT AAAAATATAA      2100
TGCAGAAAGCC AATAGAGACA AAATTTTAGC CGTAAGCTCC CAATCAGATG ATGATACGGT      2160
TATTCAATTT TGTGCAATGC ACATATTTGT TAAAGAATTG GAAGTTTGGA AACATTCAAG      2220
CACAAATGAAT AATTTCCATA TCCGTTTCGAA ATCTAGTAAA GGGATATTTT GAAGTTTAAAT      2280
AGCGCTGTTT AACACTAGAA TCTCTTATAA ACAAATTGAC ACAAATTTAA ATTCAACAAA      2340
CACCGTTCTC ATGCAAATTG ATCATGTTGT AAAGAACATT TCGGAATGTT ATAAATCTGC      2400
TTTTAAGGAT CTATCAATTA ATGTTACGCA AAATATGCAA TTTCATTCGT TCTTACAACG      2460
CATCATTGAA ATGACAGTCA GCGGTTGTCC AATTACGAAA TGTGATCCTT TAATCGAGTA      2520
TGAGGTACGA TTCACCATAT TGAATGGATT TTTGGAAAGC CTATCTTCAA ACACATCAAA      2580
ATTTAAAGAT AATATCATTC TTTTGAGAAA GGAAATTCAA CACTTGCAAG C      2631

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

Phe Phe Tyr Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe
1           5           10           15

```

```

Arg His Asp Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr
20           25           30

```

```

Phe Lys Thr Tyr Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser
35           40           45

```

```

Tyr Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys
50           55           60

```

Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala
 65 70 75 80
 Asp Glu Glu Glu Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile
 85 90 95
 Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr
 100 105 110
 Ser Phe Thr Lys Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys
 115 120 125
 Glu Phe Lys Gln Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu
 130 135 140
 Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr
 1 5 10 15
 Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp
 20 25 30
 Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu
 35 40 45
 Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro
 50 55 60
 Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
 65 70 75 80
 Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu
 85 90 95
 Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp
 100 105 110
 Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr
 115 120 125
 Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe
 130 135 140
 Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp
1          5          10          15

Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser
          20          25          30

Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu
          35          40          45

Glu Glu Glu Asn Leu Glu Lys Val Glu Glu Lys Leu Ile Pro Glu Asp
          50          55          60

Ser Phe Gln Lys Tyr Pro Gln Gly Lys Leu Arg Ile Ile Pro Lys Lys
65          70          75          80

Gly Ser Phe Arg Pro Ile Met Thr Phe Leu Arg Lys Asp Lys Gln Lys
          85          90          95

Asn Ile Lys Leu Asn Leu Asn Gln Ile Leu Met Asp Ser Gln Leu Val
          100          105          110

Phe Arg Asn Leu Lys Asp Met Leu Gly Gln Lys Ile Gly Tyr Ser Val
          115          120          125

Phe Asp Asn Lys Gln Ile Ser Glu Lys Phe Ala Gln Phe Ile Glu Lys
          130          135          140

Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Tyr Tyr Tyr Arg Lys
1          5

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Gly Lys Leu Arg Ile Ile Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Phe Arg Pro Ile Met Thr Phe
1 5

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe
1 5 10 15

Tyr Arg Lys Ser Val Trp Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu
1 5 10 15
Val Arg Gln His Arg Glu Ala
 20

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
1 5 10 15
Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1 5 10 15
Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln
 20 25

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Leu	Phe	Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly
1				5				10						15	
Ile	Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Asp	Val	Ser		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly
1				5				10						15	
Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val					
			20					25							

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Gln	Thr	Lys	Gly	Ile	Pro	Gln	Gly
1				5			

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Asp Asp Tyr Leu Leu Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

NGTNATDARD ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe
1 5 10 15

Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu
20 25 30

Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40 45

Asp Asp Tyr Leu Leu Ile Thr
50 55

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile
 1 5 10 15

Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg
 20 25 30

Val Val

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu
 1 5 10 15

Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro
 20 25 30

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
 35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Gln Lys Val Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACCRAAGG AATTCCATCA GGCTCAATTC TGTCATCTTT TTTGTGTCAT TTCTATATGG 60

AAGATTTGAT TGATGAATAC CTATCGTTTA CGAAAAGAA AGGATCAGTG TTGTTACGAG 120

TAGTCGACGA CTACCTCCTC ATCACC 146

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Lys Gly Ile Pro Ser Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe
1 5 10 15

Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys
20 25 30

Gly Ser Val Leu Leu Arg Val Val Asp Asp Tyr Leu Leu Ile Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GACGATTTC TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Asp Asp Phe Leu Phe Ile Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..35
 (D) OTHER INFORMATION: /note= "motif 0 peptide from
 Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
 1 5 10 15

Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
 20 25 30
 Asp Ile Trp
 35

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
 Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr
 1 5 10 15
 Asn Leu Arg Lys Arg Phe
 20

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..26
 (D) OTHER INFORMATION: /note= "motif 3(A) peptide from
 Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile
 1 5 10 15
 Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
1           5           10           15

Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe
          20           25           30

```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys
1           5           10           15

Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys
          20           25           30

His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn
          35           40           45

Ser

```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif 0 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
 1 5 10 15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
 20 25 30

Thr Trp

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu Phe Arg Ile
 1 5 10 15

Ile Ala Ile Pro Cys Arg Gly Ala Asp
 20 25

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	Ile
1				5					10					15	
Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys						
			20					25							

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser	Leu	Ser	Ala	Pro
1						5				10				15	
Ile	Val	Asp	Leu	Val	Tyr	Asp	Asp	Leu	Leu	Glu	Phe	Tyr	Ser	Glu	Phe
			20					25						30	

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: /note= "motif 5(C) peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln
1 5 10 15

Gln Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys
 20 25 30

Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala Val Ser Ser Gln
 35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: /note= "motif 0 peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15

Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 20 25 30

Asn Ile Trp
 35

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..23

(D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Gly	Lys	Leu	Arg	Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met
1				5					10					15	

Thr	Phe	Asn	Lys	Lys	Ile	Val
			20			

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /note= "motif 3(A) peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Lys	Leu	Phe	Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp	Ser	Val
1				5					10					15	

Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys
			20					25	

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from Euplotes aediculatus pl23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
 1 5 10 15
 Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Euplotes aediculatus pl23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu
 1 5 10 15
 Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu
 20 25 30
 Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro Leu
 35 40 45
 Ser

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 22..1716

(D) OTHER INFORMATION: /note= "EcoRI-NotI insert of
clone 712562 encoding 63 kDa
telomerase protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GCCAAAGTTCC TGC	ACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTCTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CACTTGAAGA	GGGTGCAGCT	GCGGGAGCTG	180
TGGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCG	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGARGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGCACTG	360
TTCAGCGTGC	TCAACTACGA	GCGGGCGCGG	CGCCCCGGCC	TCCTGGGCGC	CTCTGTGCTG	420
CGCCTGGACG	ATATCCACAG	GGCCTGGCGC	ACCTTCGTGC	TGCGTGTGCG	GGCCCAGGAC	480
CGCGCCCTTG	AGCTGTACTT	TGTCAAGGTG	GATGTGACGG	GCGCGTACGA	CACCATCCCC	540
CAGGACAGGC	TCACGGAGGT	CATCGCCAGC	ATCATCAAAC	CCCAGAACAC	GTA	600
CGTCGGTATG	CCGTGGTCCA	GAAGGCCGCC	ATGGGCACGT	CCGCAAGGCC	TTCAAGAGCC	660
AAGTCCTACG	TCCAGTGCCA	GGGGATCCCG	CAGGGCTCCA	TCCTCTCCAC	GCTGCTCTGC	720
AAGCTGTGCT	ACGGCGACAT	GGAGAACAAG	CTGTTTGCGG	GGATTCGGCG	GGACGGGCTG	780
CTCCTGCGTT	TGGTGGATGA	TTTCTTGTTG	GTGACACCTC	ACCTCACCCA	CGCGAAAACC	840
TTCTCAGGA	CCCTGGTCCG	AGGTGTCCCT	GAGTATGGCT	GCGTGGTGAA	CTTGCGGAAG	900
ACAGTGGTGA	ACTTCCCTGT	AGAAGACGAG	GCCCTGGGTG	GCACGGCTTT	TGTTCAGATG	960
CCGGCCCCACG	GCCTATTCCC	CTGGTGCGGC	CTGCTGCTGG	ATACCCGGAC	CCTGGAGGTG	1020
CAGAGCGACT	ACTCCAGCTA	TGCCCCGACC	TCCATCAGAG	CCAGTCTCAC	CTTCAACCGC	1080
GGCTTCAAGG	CTGGGAGGAA	CATGCGTCGC	AAACTCTTTG	GGGTCTTGCG	GCTGAAGTGT	1140
CACAGCCTGT	TTCTGGATTT	GCAGGTGAAC	AGCCTCCAGA	CGGTGTGCAC	CAACATCTAC	1200
AAGATCCTCC	TGCTGCAGGC	GTACAGGTTT	CACGCATGTG	TGCTGCAGCT	CCCATTTCAT	1260
CAGCAAGTTT	GGAAGAACCC	ACATTTTTC	TGCGCGTCAT	CTCTGACACG	GCTCCCTCTG	1320
CTACTCCATC	CTGAAAGCCA	AGAACGCAGG	GATGTCGCTG	GGGGCCAAGG	GCGCCGCCGG	1380
CCCTCTGCCC	TCCGAGGCCG	TGCAGTGGCT	GTGCCACCAA	GCATTCCTGC	TCAAGCTGAC	1440
TCGACACCGT	GTCACCTACG	TGCCACTCCT	GGGGTCACTC	AGGACAGCCC	AGACGCAGCT	1500
GAGTCGGAAG	CTCCCGGGGA	CGACGCTGAC	TGCCCTGGAG	GCCGCAGCCA	ACCCGGCACT	1560

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GCCCTCAGAC TTCAAGACCA TCCTGGACTG ATGGCCACCC GCCCACAGCC AGGCCGAGAG      1620
CAGACACCAG CAGCCCTGTC ACGCCGGGCT TATACGTCCC AGGGAGGGAG GGGCGGCCCA      1680
CACCCAGGCC TGCACCGCTG GGAGTCTGAG GCCTGAGTGA GTGTTTGGCC GAGGCCTGCA      1740
TGTCCGGCTG AAGGCTGAGT GTCCGGCTGA GGCCTGAGCG AGTGTCCAGC CAAGGGCTGA      1800
GTGTCCAGCA CACCTGCGTT TTTACTTCCC CACAGGCTGG CGTTCGGTCC ACCCCAGGGC      1860
CAGCTTTTCC TCACCAGGAG CCCGGCTTCC ACTCCCCACA TAGGAATAGT CCATCCCCAG      1920
ATTGCCCATT GTTACCCTT CGCCCTGCCT TCCTTTGCCT TCCACCCCCA CCATTTCAGGT      1980
GGAGACCCTG AGAAGGACCC TGGGAGCTTT GGAATTGG AGTGACCAA GGTGTGCCCT      2040
GTACACAGGC GAGGACCCTG CACCTGGATG GGGGTCCCTG TGGGTCAAAT TGGGGGGAGG      2100
TGCTGTGGGA GTAAAATACT GAATATATGA GTTTTTCAGT TTTGGAAAAA AAAAAAAAAA      2160
AAAAAAAAA A                                                                2171

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(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..564
- (D) OTHER INFORMATION: /note= "63 kDa telomerase protein
encoded by ORF of EcoRI-NotI insert of
clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr
1           5           10           15
Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val
20          25          30
Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val
35          40          45
Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala
50          55          60
Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp
65          70          75          80
Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr
85          90          95

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Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu Thr Ser Arg Val Lys Ala
 100 105 110
 Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu
 115 120 125
 Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr
 130 135 140
 Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe
 145 150 155 160
 Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg
 165 170 175
 Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys
 180 185 190
 Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala Met Gly Thr Ser Ala
 195 200 205
 Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 210 215 220
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 225 230 235 240
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 245 250 255
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 260 265 270
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 275 280 285
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 290 295 300
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 305 310 315 320
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 325 330 335
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 340 345 350
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 355 360 365
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 370 375 380
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 385 390 395 400
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 405 410 415

Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro
 420 425 430
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly
 435 440 445
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val
 450 455 460
 Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg
 465 470 475 480
 Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu
 485 490 495
 Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly
 500 505 510
 Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro
 515 520 525
 Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr
 530 535 540
 Thr Ser Gln Gly Gly Arg Gly Gly Pro His Pro Gly Leu His Arg Trp
 545 550 555 560
 Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
Euplotes aediculatus pl23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln
 1 5 10 15
 Lys Ser Tyr Ser Lys Thr
 20

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from
Euplotes aediculatus pl23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg	Leu	Ile	Pro	Lys	Lys
1				5				10						15	
Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys	Lys	Ile	Val		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from
Euplotes aediculatus pl23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Pro	Lys	Leu	Phe	Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp	Ser
1				5					10					15	
Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys					
			20					25							

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif B peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys
1 5 10 15

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 22

(D) OTHER INFORMATION: /note= "motif C peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile
1 5 10 15

Thr Thr Gln Glu Asn Asn
 20

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser
 1 5 10 15

Asp Leu Arg Asn Arg Thr
 20

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from
Schizosaccharomyces pombe tez1"

(2) INFORMATION FOR SEQ ID NO:276:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

(2) INFORMATION FOR SEQ ID NO:277:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile
1 5 10 15
Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
20 25

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile
 1 5 10 15

Thr Val Asn Lys Lys Asp
 20

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn Phe Ser Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser
1           5           10           15

Ser Thr Val Thr Ile Val
                20

```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 0 peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys
1           5           10           15

Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp
                20           25           30

```

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser
 1 5 10 15

Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Glu Asp Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser
 1 5 10 15

Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp
 20 25

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
 1 5 10 15

Ser Thr Asp Gln Gln Gln
 20

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Lys	Lys	Leu	Ala	Met	Gly	Gly	Phe	Gln	Lys	Tyr	Asn	Ala	Lys	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from human
telomerase core protein 1 (TCPI)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr
1				5				10					15		

Phe	Gln	Lys	Asn	Arg	Leu
				20	

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 1 5 10 15

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 20 25 30

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr
 1 5 10 15

Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile
 1 5 10 15

Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from human
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Arg Arg Asp Gly Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val
 1 5 10 15

Thr Pro His Leu Thr His
 20

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from human
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..4029
- (D) OTHER INFORMATION: /note= "preliminary sequence for human TRT cDNA insert of plasmid pGRN121"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

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GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCGATGCC      60
GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC AGCCACTACC GCGAGGTGCT      120
GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG      180
GGACCCGGCG GCTTTCGCG CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN      240
ANGGCGGCC CCCGCCGCC CCTCCTTCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC      300
CCGAGTGCTG CANANGCTGT GCGANCGCG CGCGAANAAC GTGCTGGCCT TCGGCTTCGC      360
GCTGCTGGAC GGGGCCCCG GGGGCCCCC CGAGGCCTTC ACCACCAGCG TGGCGAGCTA      420
GCTGCCCCAC ACGGTGACCG ACGCACTGCG GGGGAGCGGG GCGTGGGGG TGCTGCTGCG      480
CGGGGTGGGC GACGACGTGC TGGTTCACCT GCTGGCACGC TGGCGGNTNT TTGTGCTGGT      540
GGHTCCCAGC TGGCCCTACC ANGTTGTGCG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC      600
TCAGGCCCCG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC CAACGGGCCT      660
GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG CCAGCCCCCG GTGCGAGGAG      720
GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC      780
CCCTGAGCCG GAGCGGACGC CCGTTGGGCA GGGGTCCTGG GCCCACCCGG GCAGGACGCC      840
TGGACCGAGT GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC      900
CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG GCCGCCAGCA      960
CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT GGGACACGCC TTGTCCCCCG     1020
GTGTACGCCG AGACCAAGCA CTCCTCTAC TCCTCAGGCG ACAAGNACAC TGCGNCCCTC     1080
CTTCCTACTC AATATATCTG AGGCCCAGCC TGA CTGGCGT TCGGGAGGTT CGTGGAGACA     1140
NTCTTTCTGG TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA     1200

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GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAAACCACG CGCAGTGCCC	1260
CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT GCGGTCACCC CAGCAGCCGG	1320
TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC TGTGGCGGCC CCCGAGGAGG AGGAACACAG	1380
ACCCCCGTCTG CCTGGTGCAG CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT	1440
TCGTGCGGGC CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG	1500
AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT GCCAAGCTCT	1560
CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG CGCTTGGCTG CGCAGGAGCC	1620
CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC ACCGTCTGCG TGAGGAGATC CTGGCCAAGT	1680
TCCTGCACTG GCTGATGAGT GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA	1740
CGGAGACCAC GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT	1800
TGCAAAGCAT TGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG CTGTCCGAAG	1860
CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT GACGTCCAGA CTCCGCTTCA	1920
TCCCCAAGCC TGACGGGCTG CGGCCGATTG TGAACATGGA CTACGTCTGT GGAGCCAGAA	1980
CGTTCCGCAG AGAAAAGAGG GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG	2040
TGCTCAACTA CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG	2100
ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG GACCCGCCGC	2160
CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA CGACACCATC CCCCAGGACA	2220
GGCTCACGGA GGTTCATCGC AGCATCATCA AATCCCAGAA CACGTACTGC GTGCGTCGGT	2280
ATGCCGTGGT CCAGAAGGCC GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT	2340
CTACCTTGAC AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA	2400
GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG GCCAGCAGTG	2460
GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC CGTGCGCATC AGGGGCAAGT	2520
CCTACGTCCA GTGCCAGGGG ATCCCGCAGG GCTCCATCCT CTCCACGCTG CTCTGCAGCC	2580
TGTGCTACGG CGACATGGAG AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC	2640
TGCGTTTGGT GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC	2700
TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACCTG CGGAAGACAG	2760
TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC GGCTTTTGTG CAGATGCCGG	2820
CCCACGGCCT ATTCCCCTGG TCGGCCTGC TGCTGGATAC CCGGACCCTG GAGGTGCAGA	2880
GCGACTACTC CAGCTATGCC CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT	2940
TCAAGGCTGG GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA	3000
GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC ATCTACAAGA	3060

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TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT GCAGCTCCCA TTTCATCAGC   3120
AAGTTTGGAA GAACCCCAACA TTTTTCCTGC GCGTCATCTC TGACACGGCC TCCCTCTGCT   3180
ACTCCATCCT GAAAGCCAAG AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC   3240
CTCTGCCCTC CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC   3300
GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACCTCAG GACAGCCCAG ACGCAGCTGA   3360
GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC CGCAGCCAAC CCGGCACTGC   3420
CCTCAGACTT CAAGACCATC CTGGACTGAT GGCCACCCGC CCACAGCCAG GCCGAGAGCA   3480
GACACCAGCA GCCCTGTCAC GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC   3540
CCAGGCCCCG ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT   3600
CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA GGGCTGAGTG   3660
TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG CTCGGCTCCA CCCAGGGGCC   3720
AGCTTTTCCT CACCAGGAGC CCGGCTTCCA CTCCCCACAT AGGAATAGTC CATCCCCAGA   3780
TTCGCCATTG TTCACCCCTC GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG   3840
GAGACCCTGA GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG   3900
TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT GGGGGGAGGT   3960
GCTGTGGGAG TAAATACTG AATATATGAG TTTTTCAGTT TTGAAAAAA AAAAAAAA   4020
AAAAAAA                                         4029

```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

Ala Ala Leu Arg Pro Ala Ala His Val Gly Ser Pro Gly Pro Gly His
1           5           10           15
Pro Arg Asp Ala Ala Arg Ser Pro Leu Pro Ser Arg Ala Leu Pro Ala
20           25           30
Ala Gln Pro Leu Pro Arg Gly Ala Ala Ala Gly His Val Arg Ala Ala
35           40           45
Pro Gly Ala Pro Gly Leu Ala Ala Gly Ala Ala Arg Gly Pro Gly Gly
50           55           60

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Phe Pro Arg Xaa Gly Gly Pro Xaa Xaa Gly Val Arg Ala Leu Gly Xaa
 65 70 75 80
 Xaa Ala Ala Pro Arg Arg Pro Leu Leu Pro Pro Gly Val Leu Pro Glu
 85 90 95
 Xaa Xaa Gly Gly Pro Ser Ala Ala Xaa Ala Val Arg Xaa Arg Arg Glu
 100 105 110
 Xaa Arg Ala Gly Leu Arg Leu Arg Ala Ala Gly Arg Gly Pro Arg Gly
 115 120 125
 Pro Pro Arg Gly Leu His His Gln Arg Ala Gln Leu Pro Ala Gln His
 130 135 140
 Gly Asp Arg Arg Thr Ala Gly Glu Arg Gly Val Gly Ala Ala Ala Ala
 145 150 155 160
 Pro Arg Gly Arg Arg Arg Ala Gly Ser Pro Ala Gly Thr Leu Arg Xaa
 165 170 175
 Xaa Cys Ala Gly Gly Ser Gln Leu Arg Leu Pro Xaa Val Arg Ala Ala
 180 185 190
 Ala Val Pro Ala Arg Arg Cys Xaa Ser Gly Pro Ala Pro Ala Thr Arg
 195 200 205
 Xaa Trp Thr Arg Xaa Arg Leu Gly Ser Asn Gly Pro Gly Thr Ile Ala
 210 215 220
 Ser Gly Arg Pro Gly Ser Pro Trp Ala Ala Ser Pro Gly Cys Glu Glu
 225 230 235 240
 Ala Arg Gly Gln Cys Gln Pro Lys Ser Ala Val Ala Gln Glu Ala Gln
 245 250 255
 Ala Trp Arg Cys Pro
 260

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Ala Gly Ala Asp Ala Arg Trp Ala Gly Val Leu Gly Pro Pro Gly Gln
 1 5 10 15
 Asp Ala Trp Thr Glu
 20

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

Pro Trp Phe Leu Cys Gly Val Thr Cys Gln Thr Arg Arg Arg Ser His
1           5           10           15
Leu Phe Gly Gly Cys Ala Leu Trp His Ala Pro Leu Pro Pro Ile Arg
          20           25           30
Gly Pro Pro Ala Pro Arg Gly Pro Pro Ile His Ile Ala Ala Thr Thr
          35           40           45
Ser Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe
          50           55           60
Leu Tyr Ser Ser Gly Asp Lys Xaa Thr Ala Xaa Leu Leu Pro Thr Gln
65           70           75           80
Tyr Ile

```

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

Leu Ala Phe Gly Arg Phe Val Glu Thr Xaa Phe Leu Val Pro Gly Leu
1           5           10           15
Gly Cys Gln Asp Ser Pro Gln Val Ala Pro Pro Ala Pro Ala Xaa Leu
          20           25           30
Ala Asn Ala Ala Pro Val Ser Gly Ala Ala Trp Glu Pro Arg Ala Val
          35           40           45
Pro Leu Arg Gly Val Pro Gln Asp Ala Leu Pro Ala Ala Ser Cys Gly
          50           55           60
His Pro Ser Ser Arg Cys Leu Cys Pro Gly Glu Ala Pro Gly Leu Cys
65           70           75           80
Gly Gly Pro Arg Gly Gly Gly Thr Gln Thr Pro Val Ala Trp Cys Ser
          85           90           95

```

Cys Ser Ala Ser Thr Ala Ala Pro Gly Arg Cys Thr Ala Ser Cys Gly
 100 105 110
 Pro Ala Cys Ala Gly Trp Cys Pro Gln Ala Ser Gly Ala Pro Gly Thr
 115 120 125
 Thr Asn Ala Ala Ser Ser Gly Thr Pro Arg Ser Ser Ser Pro Trp Gly
 130 135 140
 Ser Met Pro Ser Ser Arg Cys Arg Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Ala Cys Gly Thr Ala Leu Gly Cys Ala Gly Ala Gln Gly Leu Ala Val
 1 5 10 15
 Phe Arg Pro Gln Ser Thr Val Cys Val Arg Arg Ser Trp Pro Ser Ser
 20 25 30
 Cys Thr Gly
 35

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Val Cys Thr Ser Ser Ser Cys Ser Gly Leu Ser Phe Met Ser Arg Arg
 1 5 10 15
 Pro Arg Phe Lys Arg Thr Gly Ser Phe Ser Thr Gly Arg Val Ser Gly
 20 25 30
 Ala Ser Cys Lys Ala Leu Glu Ser Asp Ser Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Arg Gly Cys Ser Cys Gly Ser Cys Arg Lys Gln Arg Ser Gly Ser Ile
 1 5 10 15
 Gly Lys Pro Gly Pro Pro Cys
 20

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg Pro Asp Ser Ala Ser Ser Pro Ser Leu Thr Gly Cys Gly Arg Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly
 1 5 10 15
 Pro Ser Val Ser Pro Arg Gly
 20